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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:55:26 ; Search time 22 Seconds

Scoring table: BLOSUM62

Title: US-09-785-474A-30

Perfect score: 2311

Sequence: 1 MTELPPRLPSYQNAQMSEDN ATDYLWQPFMDQLAQHQFVYI 467

Scoring table: GAPOP 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/2/iaa/5a_COMB.pep:*

2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/prodata/2/iaa/PCITS_COMB.pep:*

6: /cgn2_6/prodata/2/iaa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2391	100.0	467	3	US-09-706-344C-30
2	2384	99.7	467	3	US-09-706-344C-2
3	2379	99.5	467	3	US-09-706-344C-32
4	2378	99.5	467	2	US-09-967-101-134
5	2378	99.5	467	2	US-09-592-513-4
6	2378	99.5	467	3	US-09-454A-10
7	2378	99.5	467	3	US-09-670-954-2
8	2378	99.5	467	3	US-09-888-077A-2
9	2378	99.5	467	3	US-09-124-698-134
10	2378	99.5	467	3	US-09-127-480-134
11	2378	99.5	467	3	US-09-496-8841C-134
12	2378	99.5	467	4	US-09-832-867-3
13	2378	99.5	467	4	US-09-227-725A-1
14	2378	99.5	467	4	US-09-124-523-134
15	2378	99.5	467	4	US-09-375-318-3
16	2378	99.5	467	4	US-09-536-796A-134
17	2374	99.3	467	3	US-09-706-344C-4
18	2372	99.2	467	2	US-09-967-101-2
19	2372	99.2	467	2	US-09-592-541-2
20	2372	99.2	467	3	US-09-124-698-2
21	2372	99.2	467	3	US-09-127-480-2
22	2372	99.2	467	3	US-09-496-841C-2
23	2372	99.2	467	3	US-09-706-344C-28
24	2372	99.2	467	4	US-09-124-523-2
25	2372	99.2	467	4	US-09-636-796A-2
26	2372	99.2	467	4	US-09-431-048F-2
27	2368	99.0	467	4	US-09-896-621B-4

ALIGNMENTS

RESULT 1
US-09-706-344C-30

; Sequence 30, Application US/09/06344C
; Patent No. 6248555
; GENERAL INFORMATION:
; ;
; APPLICANT: TANZI, RUDOLPH
; ;
; TITLE OF INVENTION: Genetic Alterations Related To Familial
; ;
; NUMBER OF SEQUENCES: 32
; ;
; CORRESPONDENCE ADDRESS:
; ;
; ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; ;
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; ;
; CITY: WASHINGTON
; ;
; STATE: DC
; ;
; COUNTRY: USA
; ;
; ZIP: 20005-3934
; ;
; COMPUTER READABLE FORM:
; ;
; COMPUTER: IBM PC compatible
; ;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; ;
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; ;
; CURRENT APPLICATION DATA:
; ;
; APPLICATION NUMBER: US/09/706,344C
; ;
; FILING DATE: 30-AUG-1995
; ;
; CLASSIFICATION: 536
; ;
; PRIOR APPLICATION DATA:
; ;
; APPLICATION NUMBER: 60/003,054
; ;
; FILING DATE: 31-AUG-1995
; ;
; ATTORNEY/AGENT INFORMATION:
; ;
; NAME: KIM, JUDITH U.
; ;
; REGISTRATION NUMBER: 40,679
; ;
; REFERENCE/DOCKET NUMBER: 0609-4180001
; ;
; TELECOMMUNICATION INFORMATION:
; ;
; TELEPHONE: 202-771-2600
; ;
; TELEFAX: 202-371-2540
; ;
; INFORMATION FOR SEQ ID NO: 30:
; ;
; SEQUENCE CHARACTERISTICS:
; ;
; LENGTH: 467 amino acids
; ;
; TYPE: amino acid
; ;
; TOPOLOGY: linear
; ;
; MOLECULE TYPE: protein
; ;
; US-09-706-344C-30

Query Match 100.0%; Score 2391; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No 1.1e-234;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTELPPRLPSYQNAQMSEDNHLNSNTVRQDNRERQHNRSGHPEPLNSGRQGNSR 60

Db 1 MTELPAVLPSVFOAQSEDNHLISNTVRSQNDRERQHNDRSLGHPPEPLSNRPGQNSR 60

QY 61 QVVEQDEBEBELTLKYGAKKIVMFVPPVILCMVVVATKSVSVPYTRKGQLYTPTE 120

Db 61 QVVEQDEBEBELTLKYGAKKIVMFVPPVILCMVVVATKSVSVPYTRKGQLYTPTE 120

QY 121 DTETVGQRALISLNIAIMSVIVMVTILVLYKCYVIAHMLITSSLLIFFFFPPI 180

Db 121 DTETVGQRALISLNIAIMSVIVMVTILVLYKCYVIAHMLITSSLLIFFFFPPI 180

QY 181 YLGEVFTYNAVDYTVALIINFGVVGMSIHKGPLRQLQYLMISALMVFYK 240

Db 181 YLGEVFTYNAVDYTVALIINFGVVGMSIHKGPLRQLQYLMISALMVFYK 240

QY 241 LPETWTWLLAVISVVDLAVLCLKPKPLRMLVETAQERNETLPALIYSTTMWLNMAE 300

Db 241 LPETWTWLLAVISVVDLAVLCLKPKPLRMLVETAQERNETLPALIYSTTMWLNMAE 300

Db 241 YLGEVFTYNAVDYTVALIINFGVVGMSIHKGPLRQLQYLMISALMVFYK 240

QY 301 GPPEAQCRVSKNSKNAESTRESQDTVAENDGGFSEEEWAQDLSHGPRTSPESAA 360

Db 301 GPPEAQCRVSKNSKNAESTRESQDTVAENDGGFSEEEWAQDLSHGPRTSPESAA 360

QY 361 VOBLSLSSILAGEDPEERGVKUGLGDFIFSYSLVKGASATASGDWNTTACFVAILIGCL 420

Db 361 VOBLSLSSILAGEDPEERGVKUGLGDFIFSYSLVKGASATASGDWNTTACFVAILIGCL 420

QY 421 TULLAIFKKALPALPISITFGLVYFATDYLVOPFMDQAFHQFYI 467

Db 421 TULLAIFKKALPALPISITFGLVYFATDYLVOPFMDQAFHQFYI 467

RESULT 2

US-08-706-344C-2

; Sequence 2, Application US/08706344C

; Patent No. 6248555

; GENERAL INFORMATION:

; APPLICANT: TANZI, RUDOLPH

; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; TITLE OF INVENTION: Genetic Alterations Related To Familial

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; APPLICANT: TANZI, RUDOLPH

; ADDRESS: WASCO, WILMA

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/706,344C

; FILING DATE: 30-AUG-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/003,054

; FILING DATE: 31-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KIM, JUDITH U.

; REGISTRATION NUMBER: 40,679

; REFERENCE/DOCKET NUMBER: 0609.4180001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-771-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 467 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

RESULT 3

US-08-706-344C-32

; Sequence 32, Application US/08706344C

; Patent No. 6248555

; GENERAL INFORMATION:

; APPLICANT: TANZI, RUDOLPH

; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; TITLE OF INVENTION: Genetic Alterations Related To Familial

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: 60/003,054

; FILING DATE: 31-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KIM, JUDITH U.

; REGISTRATION NUMBER: 40,679

; REFERENCE/DOCKET NUMBER: 0609.4180001

; TELECOMMUNICATION INFORMATION:

US-08-706-344C-2

Query Match 99.7%; Score 2384; DB 3; Length 467;

Best Local Similarity 99.8%; Pred. No. 5.5e-234; Indels 0; Gaps 0;

Matches 465; Conservative 0; Mismatches 1; Gaps 0;

QY 1 MTELPAVLPSVFOAQSEDNHLISNTVRSQNDRERQHNDRSLGHPPEPLSNRPGQNSR 60

Db 1 MTELPAVLPSVFOAQSEDNHLISNTVRSQNDRERQHNDRSLGHPPEPLSNRPGQNSR 60

QY 61 QVVEQDEBEBELTLKYGAKKIVMFVPPVILCMVVVATKSVSVPYTRKGQLYTPTE 120

Db 61 QVVEQDEBEBELTLKYGAKKIVMFVPPVILCMVVVATKSVSVPYTRKGQLYTPTE 120

QY 121 DTETVGQRALISLNIAIMSVIVMVTILVLYKCYVIAHMLITSSLLIFFFFPPI 180

Db 121 DTETVGQRALISLNIAIMSVIVMVTILVLYKCYVIAHMLITSSLLIFFFFPPI 180

QY 181 YLGEVFTYNAVDYTVALIINFGVVGMSIHKGPLRQLQYLMISALMVFYK 240

Db 181 YLGEVFTYNAVDYTVALIINFGVVGMSIHKGPLRQLQYLMISALMVFYK 240

QY 241 LPETWTWLLAVISVVDLAVLCLKPKPLRMLVETAQERNETLPALIYSTTMWLNMAE 300

Db 241 LPETWTWLLAVISVVDLAVLCLKPKPLRMLVETAQERNETLPALIYSTTMWLNMAE 300

QY 301 GPPEAQCRVSKNSKNAESTRESQDTVAENDGGFSEEEWAQDLSHGPRTSPESAA 360

Db 301 GPPEAQCRVSKNSKNAESTRESQDTVAENDGGFSEEEWAQDLSHGPRTSPESAA 360

QY 361 VOBLSLSSILAGEDPEERGVKUGLGDFIFSYSLVKGASATASGDWNTTACFVAILIGCL 420

Db 361 VOBLSLSSILAGEDPEERGVKUGLGDFIFSYSLVKGASATASGDWNTTACFVAILIGCL 420

QY 421 TULLAIFKKALPALPISITFGLVYFATDYLVOPFMDQAFHQFYI 467

Db 421 TULLAIFKKALPALPISITFGLVYFATDYLVOPFMDQAFHQFYI 467

TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-706-344C-32

Query Match 99.5%; Score 2379; DB 3; Length 467;
Best Local Similarity 99.6%; Pred. No. 1. 8e-233; Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAULSFQNAQMSNDHNLNTRSQNDRERHNDRSLGHEPLSNGRQGNR 60

Db 1 MTELPAULSFQNAQMSNDHNLNTRSQNDRERHNDRSLGHEPLSNGRQGNR 60

QY 61 QVVEQDEBDEELTLKYGAKRVMILFVPUVTCMVVWVATIKSVFSYTRKGQLYTPTE 120

Db 61 QVVEQDEBDEELTLKYGAKRVMILFVPUVTCMVVWVATIKSVFSYTRKGQLYTPTE 120

QY 121 DTETVGQALHSINAAMISIVUWVMTLLVLYKRCYKTHAMLISSLLLFFPSI 180

Db 121 DTETVGQALHSINAAMISIVUWVMTLLVLYKRCYKTHAMLISSLLLFFPSI 180

QY 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHWKGPLRQOAYLIMISALMVFYK 240

Db 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHWKGPLRQOAYLIMISALMVFYK 240

QY 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHWKGPLRQOAYLIMISALMVFYK 240

Db 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHWKGPLRQOAYLIMISALMVFYK 240

QY 241 LPWTWAMILAVISVYDVLVACKLKGPLRQOAYLIMISALMVFYK 300

Db 241 LPWTWAMILAVISVYDVLVACKLKGPLRQOAYLIMISALMVFYK 300

QY 301 GDEPAQRVSKNSKNAESTERESQDVTAAENDGGSEEWERQDRSHLGHPRSTPESRAA 360

Db 301 GDEPAQRVSKNSKNAESTERESQDVTAAENDGGSEEWERQDRSHLGHPRSTPESRAA 360

QY 361 VQELSSSLAGDPEERGVKGIGDFTFYSVLUKGASATAGDWNTIACFVAILGLC 420

Db 361 VQELSSSLAGDPEERGVKGIGDFTFYSVLUKGASATAGDWNTIACFVAILGLC 420

QY 361 VQELSSSLAGDPEERGVKGIGDFTFYSVLUKGASATAGDWNTIACFVAILGLC 420

Db 361 VQELSSSLAGDPEERGVKGIGDFTFYSVLUKGASATAGDWNTIACFVAILGLC 420

QY 421 TULLAIFKKGALPALPISITGLVFFATDYLVQPMDFQLAFFQFYI 467

Db 421 TULLAIFKKGALPALPISITGLVFFATDYLVQPMDFQLAFFQFYI 467

RESULT 4
US-08-967-101-134

Sequence 134, Application US/08967101

Patent No. 5,440,540

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M

APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURNITZ & THIBEAUT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110

COMPUTER READABLE FORM:
COMPUTER TYPE: Floppy disk
OPERATING SYSTEM: PC-Dos/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-Nov-1997

CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/592,541

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 134:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-967-101-134

Query Match 99.5%; Score 2378; DB 2; Length 467;

Best Local Similarity 99.6%; Pred. No. 2. 2e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAULSFQNAQMSNDHNLNTRSQNDRERHNDRSLGHEPLSNGRQGNR 60

Db 1 MTELPAULSFQNAQMSNDHNLNTRSQNDRERHNDRSLGHEPLSNGRQGNR 60

QY 61 QVVEQDEBDEELTLKYGAKRVMILFVPUVTCMVVWVATIKSVFSYTRKGQLYTPTE 120

Db 61 QVVEQDEBDEELTLKYGAKRVMILFVPUVTCMVVWVATIKSVFSYTRKGQLYTPTE 120

QY 121 DTETVGQALHSINAAMISIVUWVMTLLVLYKRCYKTHAMLISSLLLFFPSI 180

Db 121 DTETVGQALHSINAAMISIVUWVMTLLVLYKRCYKTHAMLISSLLLFFPSI 180

QY 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHWKGPLRQOAYLIMISALMVFYK 240

Db 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHWKGPLRQOAYLIMISALMVFYK 240

QY 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHWKGPLRQOAYLIMISALMVFYK 240

Db 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHWKGPLRQOAYLIMISALMVFYK 240

QY 241 LPWTWAMILAVISVYDVLVACKLKGPLRQOAYLIMISALMVFYK 300

Db 241 LPWTWAMILAVISVYDVLVACKLKGPLRQOAYLIMISALMVFYK 300

QY 301 GDEPAQRVSKNSKNAESTERESQDVTAAENDGGSEEWERQDRSHLGHPRSTPESRAA 360

Db 301 GDEPAQRVSKNSKNAESTERESQDVTAAENDGGSEEWERQDRSHLGHPRSTPESRAA 360

QY 361 VQELSSSLAGDPEERGVKGIGDFTFYSVLUKGASATAGDWNTIACFVAILGLC 420

Db 361 VQELSSSLAGDPEERGVKGIGDFTFYSVLUKGASATAGDWNTIACFVAILGLC 420

QY 361 VQELSSSLAGDPEERGVKGIGDFTFYSVLUKGASATAGDWNTIACFVAILGLC 420

Db 361 VQELSSSLAGDPEERGVKGIGDFTFYSVLUKGASATAGDWNTIACFVAILGLC 420

QY 421 TULLAIFKKGALPALPISITGLVFFATDYLVQPMDFQLAFFQFYI 467

Db 421 TULLAIFKKGALPALPISITGLVFFATDYLVQPMDFQLAFFQFYI 467

RESULT 5
US-08-92-541-134

Sequence 134, Application US/08592541

Patent No. 5,946,054

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 183

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURNITZ & THIBEAUT

STREET: High Street Tower - 125 High Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

COMPUTER READABLE FORM:
COMPUTER TYPE: IBM PC compatible
OPERATING SYSTEM: PC-Dos/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/92-541-134
FILING DATE: 10-Nov-1997

Cooper

Cooper

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: Patent In Release #1.0, Version #1.30

APPLICATION NUMBER: US/08/592,541

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 134:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

STRANEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-592-541-134

Query Match 99.5%; Score 2378; DB 2; Length 467;

Best local Similarity 99.6%; Pred. No. 2.2e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAVLQFONQMSEDHLSNTVRQNDNRERQHNDRDRSIGHBPELNSRPOQNSR 60

Db 1 MTELPAVLQFONQMSEDHLSNTVRQNDNRERQHNDRDRSIGHBPELNSRPOQNSR 60

QY 61 QVQEDEEDEBELLTKYGAHKVIMFVPUVLCMVVWATKSVFSYKTRKGQLIYTPFTE 120

Db 61 QVQEDEEDEBELLTKYGAHKVIMFVPUVLCMVVWATKSVFSYKTRKGQLIYTPFTE 120

QY 121 DTETVQRALHSILMAIMSVIVMILLWVLYKRCYKVIHAWLISLLIPPSFTI 180

Db 121 DTETVQRALHSILMAIMSVIVMILLWVLYKRCYKVIHAWLISLLIPPSFTI 180

QY 181 YLGEVFKTIVNAVDYTIVALLINWFGVGMISIHKGPLRLQOQYLMISALMVFYK 240

Db 181 YLGEVFKTIVNAVDYTIVALLINWFGVGMISIHKGPLRLQOQYLMISALMVFYK 240

QY 241 LPETWTLILAVISYDVLVLCIKGPLRLVETAQERNETLPALLYSTMMVNAME 300

Db 241 LPETWTLILAVISYDVLVLCIKGPLRLVETAQERNETLPALLYSTMMVNAME 300

QY 301 GPDEAQRRVSKNSKNAESTERESQDVTVAENDGGFSEWEAQDHSIHPHRSPEAA 360

Db 301 GPDEAQRRVSKNSKNAESTERESQDVTVAENDGGFSEWEAQDHSIHPHRSPEAA 360

QY 361 VOELSSSILAGEDPERGVKGLGDFIFSVLVKASATASGDNNTIACFVAILIGCL 420

Db 361 VOELSSSILAGEDPERGVKGLGDFIFSVLVKASATASGDNNTIACFVAILIGCL 420

QY 421 TLLIAFKKALPALPISITFGLVYFATDYLVQFMDQLAFFQFYI 467

Db 421 TLLIAFKKALPALPISITFGLVYFATDYLVQFMDQLAFFQFYI 467

RESULT 6

US-08-922-4541-10

; Sequence 10: Application US/08923454A

; Patent No. 600423

; GENERAL INFORMATION:

; APPLICANT: Creasy, Caretha

; APPLICANT: Livi, George

; APPLICANT: Karran, Eric

; APPLICANT: Clinkebeard, Helen

; APPLICANT: Brown, Michael

; APPLICANT: Sotham, Christopher

TITLE OF INVENTION: HUMAN SERINE PROTEASE

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/923,454A

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 60/035436

FILING DATE: 06-SEPT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Baumolster, Kirk

REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50547

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-370-5096

TELEFAX: 610-270-5090

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

STRANEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

US-08-923-454A-10

Query Match 99.5%; Score 2378; DB 3; Length 467;

Best local Similarity 99.6%; Pred. No. 2.2e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAVLQFONQMSEDHLSNTVRQNDNRERQHNDRDRSIGHBPELNSRPOQNSR 60

Db 1 MTELPAVLQFONQMSEDHLSNTVRQNDNRERQHNDRDRSIGHBPELNSRPOQNSR 60

QY 61 QVQEDEEDEBELLTKYGAHKVIMFVPUVLCMVVWATKSVFSYKTRKGQLIYTPFTE 120

Db 61 QVQEDEEDEBELLTKYGAHKVIMFVPUVLCMVVWATKSVFSYKTRKGQLIYTPFTE 120

QY 121 DTETVQRALHSILMAIMSVIVMILLWVLYKRCYKVIHAWLISLLIPPSFTI 180

Db 121 DTETVQRALHSILMAIMSVIVMILLWVLYKRCYKVIHAWLISLLIPPSFTI 180

QY 181 YLGEVFKTIVNAVDYTIVALLINWFGVGMISIHKGPLRLQOQYLMISALMVFYK 240

Db 181 YLGEVFKTIVNAVDYTIVALLINWFGVGMISIHKGPLRLQOQYLMISALMVFYK 240

QY 241 LPETWTLILAVISYDVLVLCIKGPLRLVETAQERNETLPALLYSTMMVNAME 300

Db 226 241 LPETWTLILAVISYDVLVLCIKGPLRLVETAQERNETLPALLYSTMMVNAME 300

QY 301 GPDEAQRRVSKNSKNAESTERESQDVTVAENDGGFSEWEAQDHSIHPHRSPEAA 360

Db 301 GPDEAQRRVSKNSKNAESTERESQDVTVAENDGGFSEWEAQDHSIHPHRSPEAA 360

QY 361 VOELSSSILAGEDPERGVKGLGDFIFSVLVKASATASGDNNTIACFVAILIGCL 420

Db 361 VOELSSSILAGEDPERGVKGLGDFIFSVLVKASATASGDNNTIACFVAILIGCL 420

QY 421 TLLIAFKKALPALPISITFGLVYFATDYLVQFMDQLAFFQFYI 467

Db 421 TLLIAFKKALPALPISITFGLVYFATDYLVQFMDQLAFFQFYI 467

RESULT 7
 US 08-670-964-2
 ; Sequence 2, Application US/08670964
 ; Patent No. 6010874
 ; GENERAL INFORMATION:
 APPLICANT: Hand, John A.
 TITLE OF INVENTION: EARLY ONSET ALZHEIMER'S DISEASE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road - UW2220; P.O. Box 15
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSGC for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/670, 964
 FILING DATE: 26-JUN-1996
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 NAME: Hall, William T.
 FILING DATE: 13-JUL-1995
 APPLICATION NUMBER: 60/001, 501
 FILING DATE: 18-JUL-1995
 ATTORNEY/AGENT INFORMATION:
 TELEPHONE: 610-570-5219
 TELEFAX: 610-270-5090
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-670-964-2
 Query Match 99.5%; Score 2378; DB 3; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2.2e-233; 1; Mismatches 0; Gaps 0;
 Matches 465; Conservative 1;
 QY 1 MTELAPLISYQNAQMSEDHNLNSNTVSQDRERHNRSLGHPEPLSNRPGNSR 60
 DB 1 MTELAPLISYQNAQMSEDHNLNSNTVSQDRERHNRSLGHPEPLSNRPGNSR 60
 QY 61 QVVEQDEEDEBLTLKGAKHIVMLFVPTLQMVWVATIKSVFTRKDGQIYTPTE 120
 DB 61 QVVEQDEEDEBLTLKGAKHIVMLFVPTLQMVWVATIKSVFTRKDGQIYTPTE 120
 QY 121 DITETVGQRALHSINAAMISIVVUMTILLVLYKRYCKVTHAWLIISSLLFFSPT 180
 DB 121 DITETVGQRALHSINAAMISIVVUMTILLVLYKRYCKVTHAWLIISSLLFFSPT 180
 QY 181 YLGEGVKYNTAVDVTAVLILWNVFGVGM7SIHKGPLRQLQAYLIMLSALMVFK 240
 DB 181 YLGEGVKYNTAVDVTAVLILWNVFGVGM7SIHKGPLRQLQAYLIMLSALMVFK 240
 QY 241 LPFWTAWLILAVISVIDLAVLCKGFLRMLVETQERNNTLPALIYSTMVNLVNAE 300
 QY 121 DITETVGQRALHSINAAMISIVVUMTILLVLYKRYCKVTHAWLIISSLLFFSPT 180

RESULT 8
 US 08-888-077A-2
 ; Sequence 2, Application US/08888077A
 ; Patent No. 6020143
 ; GENERAL INFORMATION:
 APPLICANT: ST. GEORGE-HYSLOP, PETER H.
 APPLICANT: ROMMENS, JOHANNA M
 APPLICANT: FRASER, PAUL E
 TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
 TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR
 NUMBER OF SEQUENCES: 41
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
 STREET: 600 SOUTH AVENUE WEST
 CITY: WESTFIELD
 STATE: NJ
 COUNTRY: USA
 ZIP: 07090-1497
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/888, 077A
 FILING DATE: 03-JUL-1997
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 FILING DATE: 03-JUL-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PALISI, THOMAS M.
 REGISTRATION NUMBER: 36,629
 REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP CIP IV
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 654-7866
 TELEFAX: (908) 654-5000
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-888-077A-2
 Query Match 99.5%; Score 2378; DB 3; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2.2e-233; 1; Mismatches 0; Gaps 0;
 Matches 465; Conservative 1;
 QY 1 MTELAPLISYQNAQMSEDHNLNSNTVSQDRERHNRSLGHPEPLSNRPGNSR 60
 DB 1 MTELAPLISYQNAQMSEDHNLNSNTVSQDRERHNRSLGHPEPLSNRPGNSR 60
 QY 61 QVVEQDEEDEBLTLKGAKHIVMLFVPTLQMVWVATIKSVFTRKDGQIYTPTE 120
 DB 61 QVVEQDEEDEBLTLKGAKHIVMLFVPTLQMVWVATIKSVFTRKDGQIYTPTE 120
 QY 121 DITETVGQRALHSINAAMISIVVUMTILLVLYKRYCKVTHAWLIISSLLFFSPT 180
 DB 121 DITETVGQRALHSINAAMISIVVUMTILLVLYKRYCKVTHAWLIISSLLFFSPT 180
 QY 181 YLGEGVKYNTAVDVTAVLILWNVFGVGM7SIHKGPLRQLQAYLIMLSALMVFK 240
 DB 181 YLGEGVKYNTAVDVTAVLILWNVFGVGM7SIHKGPLRQLQAYLIMLSALMVFK 240
 QY 241 LPFWTAWLILAVISVIDLAVLCKGFLRMLVETQERNNTLPALIYSTMVNLVNAE 300
 QY 121 DITETVGQRALHSINAAMISIVVUMTILLVLYKRYCKVTHAWLIISSLLFFSPT 180

Db 121 DTENGQRALHSINAAMISIVUMTILLVILWLYKRYCKVTHAWLISLILLFFPSI 180
 QY 181 YLGEVFKTYNAVDYTALLINNGFGVGMISIHWKPLRQLQAYLIMISALMVALVYK 240
 Db 181 YLGEVFKTYNAVDYTALLINNGFGVGMISIHWKPLRQLQAYLIMISALMVALVYK 240
 QY 241 LPENTAWLILAVISVYDILAVLCKGPARMLVTAQERNETTPALIYSTMWLVMNAE 300
 Db 241 LPENTAWLILAVISVYDILAVLCKGPARMLVTAQERNETTPALIYSTMWLVMNAE 300
 QY 301 GDPEAQQRYSKNSKNAESTERESQDTAENDDGFSEWEAQRDLSHGPRTSPESAA 360
 Db 301 GDPEAQQRYSKNSKNAESTERESQDTAENDDGFSEWEAQRDLSHGPRTSPESAA 360
 QY 361 VQELOSSILAGEDBERGKLGQDFITSYLWVLYKASATASGWNNTIACFVAILIGCL 420
 Db 421 TLLIAFKKALPALPISITGLVYFATDYLVQPFMDQLAHQFYI 467
 Db 421 TLLIAFKKALPALPISITGLVYFATDYLVQPFMDQLAHQFYI 467

RESULT 9
 US-09-124-698-134
 Sequence 134, Application US/09124698
 Patent No. 6117578
 GENERAL INFORMATION:
 APPLICANT: ROMMENS, JOHANNA M
 TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
 NUMBER OF SEQUENCES: 183
 CORRESPONDENCE ADDRESS:
 ADDRESS: TESTA, HURWITZ & THIBEAUT
 STREET: High Street Tower - 125 High Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/124, 698
 FILING DATE:
 PRIORITY APPLICATION NUMBER: US/09/124, 698
 ATTORNEY/AGENT INFORMATION:
 NAME: Pitcher, Edmund R.
 APPLICATION NUMBER: 08/592, 541
 FILING DATE:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7100
 INFORMATION FOR SEQ ID NO: 134:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-124-698-134

Query Match 99.5%; Score 2378; DB 3; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2, 28-233;
 Matches 465; Conservative 1; Mismatches 0; Gaps 0;

1 MTELPAPIISFQNAQMSEDNHLNVRSONDNRQHNDRSLSHPEPLSNRPOANSR 50

RESULT 9
 US-09-124-698-134
 Sequence 134, Application US/09124698
 Patent No. 6117578
 GENERAL INFORMATION:
 APPLICANT: ST. GEORGE-HYSLOP, PETER H
 TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
 NUMBER OF SEQUENCES: 183
 CORRESPONDENCE ADDRESS:
 ADDRESS: TESTA, HURWITZ & THIBEAUT
 STREET: High Street Tower - 125 High Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/124, 698
 FILING DATE:
 PRIORITY APPLICATION NUMBER: US/09/124, 698
 ATTORNEY/AGENT INFORMATION:
 NAME: Pitcher, Edmund R.
 APPLICATION NUMBER: 08/592, 541
 FILING DATE:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7100
 INFORMATION FOR SEQ ID NO: 134:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

RESULT 10
 US-09-127-480-134
 Sequence 134, Application US/09127480
 Patent No. 6194193
 GENERAL INFORMATION:
 APPLICANT: ST. GEORGE-HYSLOP, PETER H
 APPLICANT: ROMMENS, JOHANNA M
 APPLICANT: FRASER, PAUL E
 TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
 NUMBER OF SEQUENCES: 183
 CORRESPONDENCE ADDRESS:
 ADDRESS: TESTA, HURWITZ & THIBEAUT
 STREET: High Street Tower - 125 High Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/127, 480
 FILING DATE:
 PRIORITY APPLICATION NUMBER: US/08/592, 541
 ATTORNEY/AGENT INFORMATION:
 NAME: Pitcher, Edmund R.
 APPLICATION NUMBER: 08/592, 541
 FILING DATE:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7100
 INFORMATION FOR SEQ ID NO: 134:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

MOLECULE TYPE: protein
US-09-127-480-134

Query Match 99.5%; Score 2378; DB 3; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2.e-233;保守
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MTELPLAPISYFQAMQSDNHLNSITVRSONDNBRERQEHNDRRSIGHPLSNGRPQNSR 60
 Db 1 MTELPLAPISYFQAMQSDNHLNSITVRSONDNBRERQEHNDRRSIGHPLSNGRPQNSR 60

INFORMATION FOR SEQ ID NO: 134
SEQUENCE CHARACTERISTICS
LENGTH: 467 amino acids
TYPE: amino acid
STRANDBONDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 134
US-08-496-841C-134

RESULT 13
US-09-227-725A-1

; Sequence 1, Application US/09227725A

; GENERAL INFORMATION:

; APPLICANT: St. George-Hyslop, Peter H.

; APPLICANT: Rommens, Johanna M.

; APPLICANT: Fraser, Paul E.

; TITLE OF INVENTION: Alzheimer's Related Proteins and Methods

; TITLE OF INVENTION: of Use

; FILE REFERENCE: 1034/1P310-US1

; CURRENT APPLICATION NUMBER: US/09/227,725A

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 467

; TEE: PRT

; ORGANISM: Homo Sapien

US-09-227-725A-1

Query Match 99.5%; Score 2378; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-233; Indels 0; Gaps 0;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAVLPSYFQNAQMSEDNHLNSNTVRSONDRQERQENDRRSLIGHPEPLSNRGPQNSR 60

Db 1 MTELPAVLPSYFQNAQMSEDNHLNSNTVRSONDRQERQENDRRSLIGHPEPLSNRGPQNSR 60

QY 61 QVVEQDEEEBELTLKYGAHVIMLFVPTLCMVVWVATKSVSFYTRKDQOLIYTPTE 120

Db 61 QVVEQDEEEBELTLKYGAHVIMLFVPTLCMVVWVATKSVSFYTRKDQOLIYTPTE 120

QY 121 DTETYGORALHSILNAMISVIVVNTILVLLVLLKRCYKVKHAWLISLSSLLFFPSI 180

Db 121 DTETYGORALHSILNAMISVIVVNTILVLLVLLKRCYKVKHAWLISLSSLLFFPSI 180

QY 181 YLGEVFKTYNAVDTVALLWNGVGMISIHWKGLRQDYLVQFMDQHOFYI 240

Db 181 YLGEVFKTYNAVDTVALLWNGVGMISIHWKGLRQDYLVQFMDQHOFYI 240

QY 241 LPENTAWLTLAVSVYDLYAVLCLKGPLMLVETAQERNETLPALIYSTMWLVNAME 300

Db 241 LPENTAWLTLAVSVYDLYAVLCLKGPLMLVETAQERNETLPALIYSTMWLVNAME 300

QY 301 GDPBPAQRVSKNSKNGNESTERESQDTAENDDGGFSEWEAORDSHGPHRSTPESRA 360

Db 301 GDPBPAQRVSKNSKNGNESTERESQDTAENDDGGFSEWEAORDSHGPHRSTPESRA 360

QY 361 VOELOSSILAGEDBERGKLGQDFIYVSVLUGKASTASAGWNTTACFVAILIGCL 420

Db 361 VOELOSSILAGEDBERGKLGQDFIYVSVLUGKASTASAGWNTTACFVAILIGCL 420

QY 421 TLLIAFKKALPALPISITFGLVYFVYFATDYLVQFMDQHOFYI 467

Db 421 TLLIAFKKALPALPISITFGLVYFVYFATDYLVQFMDQHOFYI 467

RESULT 14
US-09-124-523-134

; Sequence 134, Application US/09124523

; GENERAL INFORMATION:

; APPLICANT: St. GEORGE-HYSLOP, PETER H

; APPLICANT: ROMMENS, JOHANNA M

; APPLICANT: FRASER, PAUL E

; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

; NUMBER OF SEQUENCES: 183

; CORRESPONDENCE ADDRESS:

; ADDRESS: TESTA, HUTWITZ & THIBEAUT

; STREET: High Street Tower - 125 High Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.3.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/124.523

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/592,541

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Pitcher, Edmund R.

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100

; INFORMATION FOR SEQ ID NO: 134:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 467 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-124-523-134

Query Match 99.5%; Score 2378; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-233; Indels 0; Gaps 0;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAVLPSYFQNAQMSEDNHLNSNTVRSONDRQERQENDRRSLIGHPEPLSNRGPQNSR 60

Db 1 MTELPAVLPSYFQNAQMSEDNHLNSNTVRSONDRQERQENDRRSLIGHPEPLSNRGPQNSR 60

QY 61 QVVEQDEEEBELTLKYGAHVIMLFVPTLCMVVWVATKSVSFYTRKDQOLIYTPTE 120

Db 61 QVVEQDEEEBELTLKYGAHVIMLFVPTLCMVVWVATKSVSFYTRKDQOLIYTPTE 120

QY 121 DTETYGORALHSILNAMISVIVVNTILVLLVLLKRCYKVKHAWLISLSSLLFFPSI 180

Db 121 DTETYGORALHSILNAMISVIVVNTILVLLVLLKRCYKVKHAWLISLSSLLFFPSI 180

QY 181 YLGEVFKTYNAVDTVALLWNGVGMISIHWKGLRQDYLVQFMDQHOFYI 240

Db 181 YLGEVFKTYNAVDTVALLWNGVGMISIHWKGLRQDYLVQFMDQHOFYI 240

QY 241 LPENTAWLTLAVSVYDLYAVLCLKGPLMLVETAQERNETLPALIYSTMWLVNAME 300

Db 241 LPENTAWLTLAVSVYDLYAVLCLKGPLMLVETAQERNETLPALIYSTMWLVNAME 300

QY 301 GDPBPAQRVSKNSKNGNESTERESQDTAENDDGGFSEWEAORDSHGPHRSTPESRA 360

Db 301 GDPBPAQRVSKNSKNGNESTERESQDTAENDDGGFSEWEAORDSHGPHRSTPESRA 360

QY 361 VOELOSSILAGEDBERGKLGQDFIYVSVLUGKASTASAGWNTTACFVAILIGCL 420

Db 361 VOELOSSILAGEDBERGKLGQDFIYVSVLUGKASTASAGWNTTACFVAILIGCL 420

QY 421 TLLIAFKKALPALPISITFGLVYFVYFATDYLVQFMDQHOFYI 467

Db 421 TLLIAFKKALPALPISITFGLVYFVYFATDYLVQFMDQHOFYI 467

QY 121 DTETVGORALHSILNAIMTISVIVNTILILVLYKRCYKVIRHAWLISLJLUFFPSFI 180
 Db 121 DTETVGORALHSILNAIMTISVIVNTILILVLYKRCYKVIRHAWLISLJLUFFPSFI 180
 QY 181 YLGEVFKTIVNVAVIDYITVALLIWINFGVGMISIVMNTILVNLKRCYKVIRHAWLISLJLUFFPSFI 181
 Db 181 YLGEVFKTIVNVAVIDYITVALLIWINFGVGMISIVMNTILVNLKRCYKVIRHAWLISLJLUFFPSFI 180
 QY 241 LPETWAWLILAVIYSTIDVAVLCKGPLMLVETAQERNETLFPALYTSSTMVNLNMAE 300
 Db 241 LPETWAWLILAVIYSTIDVAVLCKGPLMLVETAQERNETLFPALYTSSTMVNLNMAE 300
 QY 241 LPETWAWLILAVIYSTIDVAVLCKGPLMLVETAQERNETLFPALYTSSTMVNLNMAE 300
 Db 301 GDEPAAQRVSKNSKNAESTERESDPTVAENDDGGFSEWEAQRDHLSGPHRSTPESRA 360
 Db 301 GDEPAAQRVSKNSKNAESTERESDPTVAENDDGGFSEWEAQRDHLSGPHRSTPESRA 360
 QY 361 VQELSSILAGEDPEERGVKLGLGDFIFPSVWVGKASATASGDWNTTACFVAILIGCL 420
 Db 361 VQELSSILAGEDPEERGVKLGLGDFIFPSVWVGKASATASGDWNTTACFVAILIGCL 420
 QY 421 TLLIAFKKALPALPISITFGLVYFATDYLVQFMDQLAHQFYI 467
 Db 421 TLLIAFKKALPALPISITFGLVYFATDYLVQFMDQLAHQFYI 467
 Db 421 TLLIAFKKALPALPISITFGLVYFATDYLVQFMDQLAHQFYI 467

RESULT 15
 US-09-375-318-3
 Sequence 3, Application US/09375318
 ; Patent No. 6468791
 GENERAL INFORMATION:
 APPLICANT: Tani, Rudolph E.
 Scheibleberg, Gerard D.
 Wasco, Wilma
 Levy-Lahid, Ephrat
 Bird, Thomas D.
 Galas, David J.

TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO
 ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:
 ADDRESSEE: SED and BEERY LLP
 STREET: 701 Fifth Ave, Suite 6300
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOSS-MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/375,318
 FILING DATE: 16-Aug-1999
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Verma, James M.
 REGISTRATION NUMBER: 33,287
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-375-318-3

Query Match Similarity 99.5%; Score 2378; DB 4; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2.2e-233;

Paul
 Flynn

Search completed: April 8, 2004, 16:59:19
 Job time : 35 secs

Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSIYQNAQMSBDEMLNSVRSQDNREFQHNRSTGHEPEPLSNGRPQNSR 60
 Db 1 MTELPAPLSIYQNAQMSBDEMLNSVRSQDNREFQHNRSTGHEPEPLSNGRPQNSR 60
 QY 61 QVVEQBEDBBLTKYGAKEVIMFVPTLCMVVNTKSVSYTRKGQLYTPFTE 120
 Db 61 QVVEQBEDBBLTKYGAKEVIMFVPTLCMVVNTKSVSYTRKGQLYTPFTE 120
 QY 121 DTETVGORALHSILNAIMTISVIVNTILILVLYKRCYKVIRHAWLISLJLUFFPSFI 180
 Db 121 DTETVGORALHSILNAIMTISVIVNTILILVLYKRCYKVIRHAWLISLJLUFFPSFI 180
 QY 181 YLGEVFKTIVNVAVIDYITVALLIWINFGVGMISIVMNTILVNLKRCYKVIRHAWLISLJLUFFPSFI 180
 Db 181 YLGEVFKTIVNVAVIDYITVALLIWINFGVGMISIVMNTILVNLKRCYKVIRHAWLISLJLUFFPSFI 180
 QY 241 LPETWAWLILAVIYSTIDVAVLCKGPLMLVETAQERNETLFPALYTSSTMVNLNMAE 300
 Db 241 LPETWAWLILAVIYSTIDVAVLCKGPLMLVETAQERNETLFPALYTSSTMVNLNMAE 300
 QY 241 LPETWAWLILAVIYSTIDVAVLCKGPLMLVETAQERNETLFPALYTSSTMVNLNMAE 300
 Db 301 GDEPAAQRVSKNSKNAESTERESDPTVAENDDGGFSEWEAQRDHLSGPHRSTPESRA 360
 Db 301 GDEPAAQRVSKNSKNAESTERESDPTVAENDDGGFSEWEAQRDHLSGPHRSTPESRA 360
 QY 361 VQELSSILAGEDPEERGVKLGLGDFIFPSVWVGKASATASGDWNTTACFVAILIGCL 420
 Db 361 VQELSSILAGEDPEERGVKLGLGDFIFPSVWVGKASATASGDWNTTACFVAILIGCL 420
 QY 421 TLLIAFKKALPALPISITFGLVYFATDYLVQFMDQLAHQFYI 467
 Db 421 TLLIAFKKALPALPISITFGLVYFATDYLVQFMDQLAHQFYI 467

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Run on:	April 9, 2004, 16:54:31 ; Search time 21 Seconds					
Scoring table:	BLOSUM62					
Gapop	10.0 , Gapext 0.5					
Searched:	283366 seqs, 96191526 residues					
Total number of hits satisfying chosen parameters:	283366					
Minimum DB seq length:	0					
Maximum DB seq length:	200000000					
Post-processing:	Maximum Match 0% listing first 45 summaries					
Database :	PIR_78,* 1: pir;* 2: pir;* 3: pir;* 4: pir;*					
Pred. No.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
Result No.	Score	Query	%	Match Length	DB ID	Description
1	2378	99.5	467	2	S58395	Presenilin 1, splice form 467 - human
2	2348	98.2	463	2	S63683	presenilin 1-463 -
3	2266	94.8	467	2	JCS5080	presenilin 1 Prote
4	2236	93.5	463	2	JCS5081	presenilin 1 Prote
5	2228	93.2	467	2	J78388	S132 protein - mou
6	2228	93.2	433	2	JCS5390	presenilin-alpha -
7	1584	65.3	374	2	S63684	presenilin 1, sp1 -
8	1462.5	61.2	449	2	JCS5391	presenilin 1 - hum
9	1444	60.4	448	2	A56993	presenilin 2 - hum
10	1376.5	57.6	442	2	J39174	seven-trans-membra
11	1054.5	44.1	836	2	B89453	protein P35H12.3 1
12	963.5	40.3	461	2	T00253	sal-12 protein - C
13	539.5	22.6	453	2	T00724	presenilin homolog
14	539	22.5	397	2	A84702	probable presenilin
15	505	21.1	358	2	T15184	presenilin-beta ho
16	309.5	12.9	465	2	T27885	spem membrane pro
17	132.5	5.5	455	2	H97237	membrane associate
18	5.0	2.386	2	739911	rad3 checkpoint pr	
19	5.0	3.09	2	H90548	hypothetical prote	
20	4.9	601	2	S12004	tyramine receptor	
21	4.8	364	2	D95959	conserved hypothet	
22	4.8	601	2	JH0170	octopamine receptor	
23	4.8	323	2	A48977	tumor surface anti	
24	4.7	339	2	G71132	hypothetical prote	
25	4.6	318	2	B84291	hypothetical prote	
26	4.6	707	2	T09340	hypothetical prote	
27	4.6	598	2	T05130	hypothetical prote	
28	4.6	599	2	T24333	hypothetical prote	
29	4.5	887	2	S73768	MG277 homolog	

30	107.5	4.5	488	2	S46118	probable glucose t
31	106	4.4	578	2	D87374	Ras G protein secretion sys
32	105.5	4.4	582	2	T43292	G protein-linked a
33	105	4.4	873	2	C90594	protein-export mem
34	104.5	4.4	486	2	H75060	hydrogenase (EC 1.
35	104.5	4.4	721	2	AH3417	lpsA protein (impo
36	104	4.3	505	2	G90419	metabolite permea
37	103.5	4.3	847	2	D84306	sodium- and chlori
38	103	4.3	846	2	T04970	probable potassium
39	102.5	4.3	470	2	T49272	hypothetical prote
40	102	4.3	1635	2	T32452	hypothetical prote
41	101.5	4.2	476	2	H89773	hypothetical prote
42	101.5	4.2	780	2	H64830	probable membrane
43	101	4.2	389	2	AB1747	cell division prot
44	101	4.2	500	2	S12899	nicotinic acetylch
45	101	4.2	553	2	D98026	hypothetical prote

ALIGNMENTS

RESULT 1	S58395	presenilin 1, splice form 467 - human
A:Alternate names:	Allzheimer's disease protein 3; protein S182	
C:Species:	Homo sapiens (man)	
C:Date:	29-Jan-1998 #sequence revision 13-Feb-1998 #text_change 29-Sep-1999	
C:Accession:	SS8396 #	
R:Sheerintton, R.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; Chi		
ero, I.; Pinesi, L.; Nee, L.; Chumakov, I.; Pollen, D.; Brookes, A.; Sanseau, P.; Poli		
E.; Rommens, J.M.; St. George-Hyslop, P.H.		
Nature 375: 754-760, 1995		
A:Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheimer		
A:Reference number: 158095; MUID:95319502; PMID:7596406		
A:Accession: SS8396		
A:Residue: 1-467 <SHE>		
A:Cross-references: EMBL:142110; NID:904118; PIDN:AB46416.1; PID:904119		
R:Vidal, R.; Ghiso, J.; Wisniewski, T.; Frangione, B.		
FEBS Lett. 393: 19-23, 1996		
A:Title: Alzheimer's presenilin 1 gene expression in platelets and megakaryocytes. Ider		
A:Reference number: S71401; MUID:6339721; PMID:8804415		
A:Accession: S71401		
A:Status: not compared with conceptual translation		
A:Molecule type: mRNA		
A:Residues: 24-32;24-256;290-292;316-17;376-379 <VIV>		
A:Experimental source: Dani megakaryotic cell line (ATCC CRL-9792) and platelets		
C:Genetics:		
A:Gene: GDB:PS8M1; AD3; FAD; S182; PSI		
A:Cross-references: GDB:135692; OMIM:104311		
A:Map position: 14q4.3-14q24.3		
C:Superfamily: alternative splicing; Alzheimer's disease; glycoprotein; transmembrane protein		
F:82-00/Domain: transmembrane #status predicted <TM1>		
F:82-00/Domain: transmembrane #status predicted <TM2>		
F:133-154/Domain: transmembrane #status predicted <TM3>		
F:164-185/Domain: transmembrane #status predicted <TM4>		
F:195-211/Domain: transmembrane #status predicted <TM5>		
F:221-238/Domain: transmembrane #status predicted <TM6>		
F:244-264/Domain: transmembrane #status predicted <TM7>		
F:281-301/Domain: transmembrane #status predicted <TM8>		
F:408-428/Domain: transmembrane #status predicted <TM9>		
F:433-453/Domain: transmembrane #status predicted <TM10>		
F:279,405/Binding site: carbohydrate (Asn) (covalent) #status predicted		
Query Match 99.5%; Score 2378; DB 2; Length 467;		
Best Local Similarity 99.6%; Pred. No. 1.3e-17; I		
Matches 465; Conservative 1; Mismatches 0; Gaps 0;		
QY 1 MTELPAVLPSYFONAQMSEDNLNTVRSQNDRERQHNDRSRIGHPESLNSGRQNSR 60		
Db 1 MTELPAVLPSYFONAQMSEDNLNTVRSQNDRERQHNDRSRIGHPESLNSGRQNSR 60		
OY 61 QVVEQFEDDEBLTILKXGAKHIVMLFPVILCMVVVATKSVSYTRKGQOLIVTPFE 120		

Db 61 QVEQDDEDEBILTLKGAKVIMLFPVTPGMVVVATIKSVFTRKGQLIYTPFTE 120

QY 121 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 180

Db 121 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 180

QY 181 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 240

Db 181 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 240

QY 241 LPENTWALILAVISVYDILAVICLKGPLRMLYETAQERNETLPALIYSSTMWLNMAE 300

Db 241 LPENTWALILAVISVYDILAVICLKGPLRMLYETAQERNETLPALIYSSTMWLNMAE 300

C;Accession: S63683 Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999

R;Sahara, N.; Yahagi, Y.; Takagi, H.; Kondo, T.; Okochi, M.; Usami, M.; Shirasawa, T.; Y; FEBs Lett. 381: 7-11, 1996

A;Title: Identification and characterization of presenilin 1-467, 1-463 and 1-374.

A;Reference number: S63683; NUID:96193901; PMID:8641442

A;Accession: S63683

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

C;Specie: Homo sapiens (man)

C;Cross-references: EMBL:Z71333; NID:51707591; PIDN:CAA95930.1; PID:91707592

C;Superfamily: presenilin

C;Keywords: transmembrane protein

F;82/10/Domain: transmembrane #status predicted <TM1>

F;133-154/Domain: transmembrane #status predicted <TM2>

F;164-185/Domain: transmembrane #status predicted <TM3>

F;195-213/Domain: transmembrane #status predicted <TM4>

F;221-238/Domain: transmembrane #status predicted <TM5>

F;244-261/Domain: transmembrane #status predicted <TM6>

F;408-428/Domain: transmembrane #status predicted <TM7>

Query Match 98 %; Score 2348; DB 2; Length 463;

Matches 461; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

Best Local Similarity 98.7%; Pred. No. 2.9e-175;

Query Match 94.8%; Score 2266; DB 2; Length 467;

Matches 442; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Query Match 94.6%; Score 2169; DB 2; Length 469;

Matches 442; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Db 1 MTELAPLISYQNAQNSEDNHLNTRSQNDRERQEHNRSLGHPEPLSNGRPGNSR 60

Db 1 MTELAPLISYQNAQNSEDNHLNTRSQNDRERQEHNRSLGHPEPLSNGRPGNSR 60

QY 61 QVVEQDDEDEBILTLKGAKVIMLFPVTPGMVVVATIKSVSITRKGQLIYTPFTE 120

Db 61 QVVEQDDEDEBILTLKGAKVIMLFPVTPGMVVVATIKSVSITRKGQLIYTPFTE 120

Db 121 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 180

QY 121 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 180

Db 117 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 176

QY 117 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 176

Db 181 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 240

QY 181 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 240

Db 177 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 236

QY 177 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 236

Db 241 LPENTWALILAVISVYDILAVICLKGPLRMLYETAQERNETLPALIYSSTMWLNMAE 300

QY 241 LPENTWALILAVISVYDILAVICLKGPLRMLYETAQERNETLPALIYSSTMWLNMAE 300

Db 237 LPENTWALILAVISVYDILAVICLKGPLRMLYETAQERNETLPALIYSSTMWLNMAE 296

QY 301 GDEBAQRVSKNSKNAESTERSQDVTVAENDGGSSEMERQDRSHLGPHTPSRAA 360

Db 301 GDEBAQRVSKNSKNAESTERSQDVTVAENDGGSSEMERQDRSHLGPHTPSRAA 360

QY 361 VQELSSSLAGEDPEERGVKLGGDFTFYSVIYKRCYKASATASDMDNTIACFVAILIGCL 420

Db 361 VQELSSSLAGEDPEERGVKLGGDFTFYSVIYKRCYKASATASDMDNTIACFVAILIGCL 420

Db 421 TLLIAIFKKAALPISITFGVLYFVYFATDYLVQPFMDQLAHQFYI 467

Db 421 TLLIAIFKKAALPISITFGVLYFVYFATDYLVQPFMDQLAHQFYI 467

RESULT 2

S63683 presenilin 1-463 - human

C;Accession: S63683 Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 20-Jun-2000

R;Calenda, A.; Mestre-Francés, N.; Czech, C.; Pradier, L.; Petter, A.; Bons, N.; Bellis, Biochem. Biophys. Res. Commun. 228, 430-435, 1996

A;Title: Molecular cloning, sequencing, and brain expression of the presenilin 1 gene in the mouse

A;Reference number: JC5080; NID:97079199; PMID:8920931

A;Accession: JC5080

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-467 <CAL>

A;Cross-references: EMBL:Z71333; NID:51707591; PIDN:CAA95930.1; PID:91707592

A;Experimental source: brain

C;Comments: This protein is an integral membrane protein with seven transmembrane domains

C;Genetics:

A;Gene: ps1

A;Map position: 14

C;Superfamily: presenilin

F;82/10/Domain: transmembrane #status predicted <TM1>

F;133-154/Domain: transmembrane #status predicted <TM2>

F;164-185/Domain: transmembrane #status predicted <TM3>

F;195-213/Domain: transmembrane #status predicted <TM4>

F;221-238/Domain: transmembrane #status predicted <TM5>

F;244-261/Domain: transmembrane #status predicted <TM6>

F;408-428/Domain: transmembrane #status predicted <TM7>

Query Match 94.8%; Score 2266; DB 2; Length 467;

Matches 442; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Query Match 94.6%; Score 2169; DB 2; Length 469;

Matches 442; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Db 1 MTELAPLISYQNAQNSEDNHLNTRSQNDRERQEHNRSLGHPEPLSNGRPGNSR 60

Db 1 MTELAPLISYQNAQNSEDNHLNTRSQNDRERQEHNRSLGHPEPLSNGRPGNSR 60

QY 61 QVVEQDDEDEBILTLKGAKVIMLFPVTPGMVVVATIKSVSITRKGQLIYTPFTE 120

Db 61 QVVEQDDEDEBILTLKGAKVIMLFPVTPGMVVVATIKSVSITRKGQLIYTPFTE 120

Db 121 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 180

QY 121 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 180

Db 177 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 176

QY 177 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 176

Db 181 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 240

QY 181 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 240

Db 181 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 240

Db 241 LPENTWALILAVISVYDILAVICLKGPLRMLYETAQERNETLPALIYSSTMWLNMAE 300

QY 241 LPENTWALILAVISVYDILAVICLKGPLRMLYETAQERNETLPALIYSSTMWLNMAE 300

Db 301 GDEBAQRVSKNSKNAESTERSQDVTVAENDGGSSEMERQDRSHLGPHTPSRAA 360

QY 301 GDEBAQRVSKNSKNAESTERSQDVTVAENDGGSSEMERQDRSHLGPHTPSRAA 360

Db 361 VQELSSSLAGEDPEERGVKLGGDFTFYSVIYKRCYKASATASDMDNTIACFVAILIGCL 420

Db 361 VQELSSSLAGEDPEERGVKLGGDFTFYSVIYKRCYKASATASDMDNTIACFVAILIGCL 420

Db 421 TLLIAIFKKAALPISITFGVLYFVYFATDYLVQPFMDQLAHQFYI 467

Db 421 TLLIAIFKKAALPISITFGVLYFVYFATDYLVQPFMDQLAHQFYI 467

RESULT 3

JC5080 presenilin 1 protein isoform 467 - lesser mouse lemur

C;Species: Microcebus murinus (lesser mouse lemur)

C;Accession: JC5080

R;Calenda, A.; Mestre-Francés, N.; Czech, C.; Pradier, L.; Petter, A.; Bons, N.; Bellis, Biochem. Biophys. Res. Commun. 228, 430-435, 1996

A;Title: Molecular cloning, sequencing, and brain expression of the presenilin 1 gene in the mouse

A;Reference number: JC5080; NID:97079199; PMID:8920931

A;Accession: JC5080

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-467 <CAL>

A;Cross-references: EMBL:Z71333; NID:51707591; PIDN:CAA95930.1; PID:91707592

A;Experimental source: brain

C;Comments: This protein is an integral membrane protein with seven transmembrane domains

C;Genetics:

A;Map position: 14

C;Superfamily: presenilin

F;82/10/Domain: transmembrane protein

F;133-154/Domain: transmembrane #status predicted <TM1>

F;164-185/Domain: transmembrane #status predicted <TM2>

F;195-213/Domain: transmembrane #status predicted <TM3>

F;221-238/Domain: transmembrane #status predicted <TM4>

F;244-261/Domain: transmembrane #status predicted <TM5>

F;408-428/Domain: transmembrane #status predicted <TM6>

Query Match 94.8%; Score 2266; DB 2; Length 467;

Matches 442; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Query Match 94.6%; Score 2169; DB 2; Length 469;

Matches 442; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Db 1 MTELAPLISYQNAQNSEDNHLNTRSQNDRERQEHNRSLGHPEPLSNGRPGNSR 60

Db 1 MTELAPLISYQNAQNSEDNHLNTRSQNDRERQEHNRSLGHPEPLSNGRPGNSR 60

QY 61 QVVEQDDEDEBILTLKGAKVIMLFPVTPGMVVVATIKSVSITRKGQLIYTPFTE 120

Db 61 QVVEQDDEDEBILTLKGAKVIMLFPVTPGMVVVATIKSVSITRKGQLIYTPFTE 120

Db 121 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 180

QY 121 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 180

Db 177 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 176

QY 177 DPTVGORALHSINNAIMISIVMNTILVVLVLYKRCYKIHAWLISSLLUFFPSFI 176

Db 181 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 240

QY 181 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 240

Db 181 YIGEVFKYIVNADYITVALLWNFGVGMISIHKGPLRQOAYLIMISALMVFYK 240

Db 241 LPENTWALILAVISVYDILAVICLKGPLRMLYETAQERNETLPALIYSSTMWLNMAE 300

QY 241 LPENTWALILAVISVYDILAVICLKGPLRMLYETAQERNETLPALIYSSTMWLNMAE 300

Db 301 GDEBAQRVSKNSKNAESTERSQDVTVAENDGGSSEMERQDRSHLGPHTPSRAA 360

QY 301 GDEBAQRVSKNSKNAESTERSQDVTVAENDGGSSEMERQDRSHLGPHTPSRAA 360

Db 361 VQELSSSLAGEDPEERGVKLGGDFTFYSVIYKRCYKASATASDMDNTIACFVAILIGCL 420

Db 361 VQELSSSLAGEDPEERGVKLGGDFTFYSVIYKRCYKASATASDMDNTIACFVAILIGCL 420

Db 421 TLLIAIFKKAALPISITFGVLYFVYFATDYLVQPFMDQLAHQFYI 467

Db 421 TLLIAIFKKAALPISITFGVLYFVYFATDYLVQPFMDQLAHQFYI 467

Db 421 TILLIAFKKALPALPISITGLVVFATDYLVQPFMDQLAHQFYI 467

RESULT 4

C;Species: Mus musculus (house mouse)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 29-Sep-1999
C;Accession: I7388

JC5081 presenilin 1 protein isoform 463 - lesser mouse lemur
C;Species: Microcebus murinus (lesser mouse lemur)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Sep-1998
C;Accession: JC5081
R;Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Petter, A.; Bons, N.; Bellis, Biochem. Biophys. Res. Commun. 228, 430-439, 1996
A;Title: Molecular cloning, sequencing, and brain expression of the presenilin 1 gene in
A;Reference number: JC5080; MUID:97079199; PMID:8920931
A;Contents: brain
A;Accession: JC5081
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-463 <CUL>
A;Cross-references: EMBL:27133
C;Comment: This protein is an intermembrane protein with seven transmembrane domains.
C;Genetics:
A;Gene: ps1
A;Map position: 14
C;Superfamily: presenilin
C;Keywords: transmembrane protein
F;78-96/Domain: transmembrane #status predicted <TM1>
F;129-150/Domain: transmembrane #status predicted <TM2>
F;160-181/Domain: transmembrane #status predicted <TM3>
F;191-209/Domain: transmembrane #status predicted <TM4>
F;217-234/Domain: transmembrane #status predicted <TM5>
F;240-257/Domain: transmembrane #status predicted <TM6>
F;404-424/Domain: transmembrane #status predicted <TM7>

Query Match 93.2%; Score 228; DB 2; Length 467;
Best Local Similarity 93.2%; Pred. No. 6.5e-166; Indels 0; Gaps 0;
Matches 431; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MTEJPAPLSYFQNAQMSEDNHLSNTRSQNDRERHNRSLGHPEPLSNGRQGNSR 60
Db 1 MTEJPAPLSYFQNAQMSEDNHLSNTRSQNDRERHNRSLGHPEPLSNGRQGNSR 60

Qy 61 QVVEQDEBEDELTLKYGAKEVIMLFVPUVTLCMVWVATKSVSFYTRKGQLIYTPTE 120
Db 61 QVVEQDEBEDELTLKYGAKEVIMLFVPUVTLCMVWVATKSVSFYTRKGQLIYTPTE 120

Qy 121 DTTVSGRALISLNKAMISVIVWNTLWLYKRCYKTHAMLIISLILLUFFFSI 180
Db 121 DTTVSGRALISLNKAMISVIVWNTLWLYKRCYKTHAMLIISLILLUFFFSI 180

Qy 181 YLGEVEKTYNVAVDYTVALLIWNGVGMISIHWKGPLRQLQAVLIMMSALMVFKY 240
Db 181 YLGEVEKTYNVAVDYTVALLIWNGVGMISIHWKGPLRQLQAVLIMMSALMVFKY 240

Qy 241 LPWTAWLILAVISVDIWLCKGPIRMLVETQERNSTLPALIYSTMMWLNMAE 300
Db 241 LPWTAWLILAVISVDIWLCKGPIRMLVETQERNSTLPALIYSTMMWLNMAE 300

Qy 301 GDEPAQRVSKNSKAESTERESDQTVAAENDDGGPSEWEAQDRSHGHRSPESRAA 360
Db 301 GDEPAQRVSKNSKAESTERESDQTVAAENDDGGPSEWEAQDRSHGHRSPESRAA 360

Qy 361 YOELSSSILAGEDPBERGVKGGLGDFIFSYSTVKGASATASGDWNTTACFVAILIGCL 420
Db 361 YOELSSSILAGEDPBERGVKGGLGDFIFSYSTVKGASATASGDWNTTACFVAILIGCL 420

Qy 421 TILLIAFKKALPALPISITGLVVFATDYLVQPFMDQLAHQFYI 467
Db 421 TILLIAFKKALPALPISITGLVVFATDYLVQPFMDQLAHQFYI 467

RESULT 6

JC5390 presenilin-alpha - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C;Accession: JC5390
R;Tsujimura, A.; Yaeojima, K.; Hasimoto-Gotoh, T.
Biochem. Biophys. Res. Commun. 231, 392-396, 1997
A;Title: Cloning of Xenopus presenilin-alpha and -beta cDNAs and their differential exp.
A;Reference number: JC5390; MUID:9722465; PMID:9070286
A;Accession: JC5390
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-13 <TSU>
A;Cross-references: DDBJ:D84427; NID:9194353; PID:BA19570.1; PID:9194354
A;Experimental source: brain
C;Comment: This protein plays a role in negative regulation of apoptotic cascades during
C;Superfamily: presenilin
F;48-66/Domain: transmembrane #status predicted <TM1>
F;99-119/Domain: transmembrane #status predicted <TM2>

RESULT 5

I7888 protein - mouse

RESULT 5

I7888 protein - mouse

Db 307 MAD-SATADGRMNQVQHIDRNTPEGANSTV-----ED 338
 Qy 358 RAAVQELSSILAGEDP-T-ERGVKUGLGPPIFYSVLUKGASATASGDNTTACFVAILIGCLT 402
 Db 339 AETIQTQDNTLSPDDERGVKGPIFYSVLUKGASATASGDNTTACFVAILI 398
 Qy 417 GICLTULLAIAFKKALPALPISITGLVYFATDYLVQPFMDQLAFFQFYI 467
 Db 399 GICLTULLAIAFKKALPALPISITGLVYFATDYLVQPFMDQLAFFQFYI 449

RESULT 9
 A5693
 presenilin 2 - human
 N;Alternate names: Alzheimer's disease protein 4
 C;Species: Homo sapiens (man)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Nov-2000
 C;Accession: A5693; 18098
 R;Ievy-Lahad, E.; Wasco, W.; Pooraj, P.; Romano, D.M.; Oshima, J.; Pettingell, W.H.; Yu, Science 269, 973-977, 1995
 A;Title: Candidate gene for the chromosome 1 familial Alzheimer's disease locus.
 A;Reference number: A5693; MUID:9536816; PMID:7636622
 A;Accession: A5693
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Residues: 1-448 <RES>
 A;Cross-references: GB:I43964; NID:951202; PIDN:AA859557.1; PID:951203
 R;Rogaev, E.I.; Sherrington, R.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; Liang, Y.; Chi, J.; Cohen, D.; Hannett, L.; Fraser, P.E.; Rommens, J.M.; St George-Hyslop, P.H.
 Nature 376, 775-778, 1995
 A;Title: Familial Alzheimer's disease in kindreds with missense mutations in a gene on chromosome 1
 A;Accession: I58098; MUID:9539971; PMID:7651536
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Cross-references: GDB:SEN2; AD4; STM2; PS2; E5-1
 A;Cross-references: GDB:633044; OMIM:600759
 A;Map position: 1q31-1q42
 C;Supergroup: presenilin
 Query Match 60.4%; Score 1444; DB 2; Length 448;
 Best Local Similarity 57.6%; Pred. No. 1.4e-99;
 Matches 286; Conservative 40; Mismatches 82; Indels 41; Gaps 6;
 Matches 303; Conservative 40; Mismatches 81; Indels 42; Gaps 8;
 Qy 3 ELPAPISYFQNAQMSDNHNTVSQNDRERHNDR-SLGHEPLSNRPOGNSRQ 61
 Db 24 ESPTPRSCQEGRQGPEDGENTAQWQSNQENBDSEDPDRYVCSGP----GRPPG--- 74
 Qy 62 WVEQDDEBDELTKYGAKEVIMLUPVILQMVWATKSVSYTRKQQLIVPTED 121
 Db 75 -----LEEBELTKYGAKEVIMLUPVILQMVWATKSVSYTRKQQLIVPTED 127
 Qy 122 TETVGORALHSILNAIMISVWVMTLILVLYKRCYVTHAMILTISIILUPFSFIY 181
 Db 128 TPSVQRLNLNSVNLNTLIMISVWVMTLILVLYKRCYVHLMSMILFITY 187
 Qy 182 LGEVFKTINYVNAVDYITVVALIWNFGVGVMSIHKGKPLRQQLQYALIMISALMVFVKKL 241
 Db 183 LGEVFKTINYVNAVDYITVVALIWNFGVGVMSIHKGKPLRQQLQYALIMISALMVFVKKL 247
 Qy 184 PEWTWILILAVTSDVAVLCKPLRMLVETQERNLTFLPALLYSTTMWVLYNMAEG 301
 Db 248 PEWSAWVILGAISSVVDLAVLCKPKGLRMLVETQERNSPIPPALYSSANWVTVGMAKL 307
 Qy 302 DPEAQRRVSKNSKHAESTERESQDVTVAENDGGERSEREAQRSHLGHFRSTBESRAV 361
 Db 308 DPSSQALQ-----PYPMEMDSYDSFGEPSPYEPVBRPLTGPG----- 348
 Qy 362 QBLSSILAGEDPPERGVKGPIFYSVLUKGASATASGDNTTACFVAILIGCLT 421
 Db 349 EEELEB---EEESOGGVKGPIFYSVLUKGASATASGDNTTACFVAILIGCLT 403
 Qy 422 LLLIAIAFKKALPALPISITGLVYFATDYLVQPFMDQLAFFQFYI 450
 Db 404 LLLIAIAFKKALPALPISITGLVYFATDYLVQPFMDQLAFFQFYI 432

RESULT 10
 139174
 seven trans-membrane domain protein AD3LP/ADS - human
 C;Accession: I39174
 C;Species: Homo sapiens (man)
 C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 29-Sep-1999
 C;Accession: I39174
 R;Li, J.; Mai, J.; Potter, H.
 Proc. Natl. Acad. Sci. U.S.A. 92, 12180-12184, 1995
 A;Title: Identification and expression analysis of a potential familial Alzheimer's disease gene
 A;Reference number: I39174; MUID:9109229; PMID:8618867
 A;Accession: I39174
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-42 <RBS>
 A;Cross-references: EMBL:U34349; NID:91079375; PIDN: AAC50290.1; PID:91079576
 C;Superfamily: presenilin
 Query Match 57.6%; Score 1376.5; DB 2; Length 442;
 Best Local Similarity 53.7%; Pred. No. 1.4e-99;
 Matches 286; Conservative 40; Mismatches 82; Indels 41; Gaps 6;
 Matches 286; Conservative 40; Mismatches 82; Indels 41; Gaps 6;
 Qy 3 ELPAPISYFQNAQMSDNHNTVSQNDRERHNDR-SLGHEPLSNRPOGNSRQ 61
 Db 24 ESPTPRSCQEGRQGPEDGENTAQWQSNQENBDSEDPDRYVCSGP----GRPPG--- 74
 Qy 62 WVEQDDEBDELTKYGAKEVIMLUPVILQMVWATKSVSYTRKQQLIVPTED 121
 Db 75 -----LEEBELTKYGAKEVIMLUPVILQMVWATKSVSYTRKQQLIVPTED 127
 Qy 122 TETVGORALHSILNAIMISVWVMTLILVLYKRCYVTHAMILTISIILUPFSFIY 181
 Db 128 TPSVQRLNLNSVNLNTLIMISVWVMTLILVLYKRCYVHLMSMILFITY 187
 Qy 182 LGEVFKTINYVNAVDYITVVALIWNFGVGVMSIHKGKPLRQQLQYALIMISALMVFVKKL 241
 Db 183 LGEVFKTINYVNAVDYITVVALIWNFGVGVMSIHKGKPLRQQLQYALIMISALMVFVKKL 247
 Qy 184 PEWTWILILAVTSDVAVLCKPLRMLVETQERNLTFLPALLYSTTMWVLYNMAEG 301
 Db 248 PEWSAWVILGAISSVVDLAVLCKPKGLRMLVETQERNSPIPPALYSSANWVTVGMAKL 307
 Qy 302 DPEAQRRVSKNSKHAESTERESQDVTVAENDGGERSEREAQRSHLGHFRSTBESRAV 361
 Db 308 DPSSQALQ-----PYPMEMDSYDSFGEPSPYEPVBRPLTGPG----- 348
 Qy 362 QBLSSILAGEDPPERGVKGPIFYSVLUKGASATASGDNTTACFVAILIGCLT 421
 Db 349 EEELEB---EEESOGGVKGPIFYSVLUKGASATASGDNTTACFVAILIGCLT 403
 Qy 422 LLLIAIAFKKALPALPISITGLVYFATDYLVQPFMDQLAFFQFYI 450
 Db 404 LLLIAIAFKKALPALPISITGLVYFATDYLVQPFMDQLAFFQFYI 432

RESULT 11
 E89453
 Protein F35H12.3 [imported] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
 C;Accession: E89453
 R;anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
 A;Reference number: A75000; MUID:906913; PMID:98516
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/ for published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: E89453
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-835 <SPO>
 A;Cross-references: GB:chr X; PIDN:AAA83176.1; PID:9109863; GSPDB:GN00028; CESP:F35H12.
 C;Note: similar to M. musculus S182 protein (GB:J42177)
 A;Gene: F35H12.3
 A;Map position: X

Query Match 44.1%; Score 1054.5; DB 2; Length 836; Best Local Similarity 50.9%; Pred: No. 3; 5e-74; Mismatches 216; Conservative 70; Indels 43; Gaps 6; Matches 152

64 EDEDEDEBELTUKYGAHKVIMLFPVTLCMVVVATIKSVSEYTRKQGQ-LIYTPFEDT 122
 32 QEDENVVVEEAEALKYGAHSHVTHLFVPUVSLCMALVUFTNTTITYPSQNRGRHLVYTPFRET 91

123 ETYGQRALHSLNAAIMTSVIVMILWVLYKRCYKVIHAWLISLUFFSSPIYL 182
 92 DSTVEKGMSLGMISLGMALVWLMCUCWVUMLTIVYKPYKVKLIGHLWLSFLFLFTIYV 151

183 GEVFKTYNAVDVITVALLIWFNGVGMISIHWKGPRQQLQYLMISALMAVLYKYL 242
 152 QEVLKSFDVPSALLVFLPGLGNYGULGMCMCITHKGKGLRQLQYLMISALMAVLYKYL 211

243 EWTAWLILAVIATSYDVLAVLCLKGPRMLVETAQERNETLPALITYSSTMWV--LYNMA 299
 212 EWTWVFVLFVISWDLVAVLTPKGPRLYVETAQERNEPFPLAIVYVYVWLTAV 271

300 EGDPEPAGRRVSKS-----KHNAASTERRSQDTVAENDDGFS 337
 272 ENTTDPREPTSSDSNTSTAFFGEASCSETPKPKVRIPOVQVINSNTTASTQNSGVR 331

338 ESEWEAQRDSHLGHRSIPESRAVQELSSSILAGEDEBERGKLGDFIYVNGKAS 397
 332 VE-----RELAERPTVODAN--FHRHEBERGVKGJGDFIYVNGKAS 376

398 ATASGDWNTTIAFPVAILGLCJTLIAIFKCALPALPISITPGLUVYP 447
 377 SYF--DWNTTIACTVAILGLCFTLVLLAVFKALPALQFPRFSPDSFTP 424

Db 92 DSVKEKGMSLGMISLGMALVWLMCUCWVUMLTIVYKPYKVKLIGHLWLSFLFLFTIYV 151
 QY 183 GEVFKTYNAVDVITVALLIWFNGVGMISIHWKGPRQQLQYLMISALMAVLYKYL 242
 Db 152 QEVLKSFDVPSALLVFLPGLGNYGULGMCMCITHKGKGLRQLQYLMISALMAVLYKYL 211
 QY 243 EWTAWLILAVIATSYDVLAVLCLKGPRMLVETAQERNETLPALITYSSTMWV--LYNMA 299
 Db 212 EWTWVFVLFVISWDLVAVLTPKGPRLYVETAQERNEPFPLAIVYVYVWLTAV 271
 QY 300 EGDPEPAGRRVSKS-----KHNAASTERRSQDTVAENDDGFS 337
 Db 272 ENTTDPREPTSSDSNTSTAFFGEASCSETPKPKVRIPOVQVINSNTTASTQNSGVR 331
 QY 338 ESEWEAQRDSHLGHRSIPESRAVQELSSSILAGEDEBERGKLGDFIYVNGKAS 397
 Db 332 VE-----RELAERPTVODAN--FHRHEBERGVKGJGDFIYVNGKAS 376
 QY 398 ATASGDWNTTIAFPVAILGLCJTLIAIFKCALPALPISITPGLUVYP 447
 Db 377 SYF--DWNTTIACTVAILGLCFTLVLLAVFKALPALQFPRFSPDSFTP 424

RESULT 13
 T00724
 presenilin homolog F22013.19 - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
 C;Accession: T00724
 R;Shin, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Colognesi, A.; Ecker, J.R.; submitted to the EMBL Data Library, April 1998
 A;Description: Genomic sequence for *Arabidopsis thaliana* BAC F22013.
 A;Reference number: Z14200
 A;Accession: T00724
 A;Stratoc: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-453 <SHT>
 A;Cross-references: EMBL:AC003981; NRD:93063439; PID:93063457; GSPDB:GN00059; ATSP:F22013
 A;Experimental source: cultivar Columbia
 C;Genetics:
 A;Gene: ATSP:F22013.19
 A;Map position: 1
 A;Introns: 1081
 C;Superfamily: presenilin

Query Match 22.6%; Score 539.5; DB 2; Length 453; Best Local Similarity 33.0%; Pred: No. 2; 3e-34; Mismatches 145; Conservative 19; Indels 71; Gaps 14; Matches 131

82 VMLFVPUVTCMWWVWATIKSVSEYTRKQGQ-LIYTPFEDT 137
 13 IGMWAPVSIWCMFLVWLTYSLSVSDPQIRSAANLIVENPSDSTV--KLEGSLNAT 70

138 IMISVIVMILWVLYKRCYKVIHAWLISLUFFSSPIYLGEVKTYNAVDY 197
 71 VFWVLLIAVFTVILPFLYVYFTNPLKHYMFSAFLVGLGAGFLSIIQHFSIYVDSIT 130

198 VALLIWFNGVGMISIHWKG_PLRQQLQYLMISALMAVLYKYLPEWPAWLLAVIY 256
 131 CFTLLEPNFTTGTLSLVPAGGIPVIRQCYKVMGIVVAAWFTK_LPEWTFWFLVALY 189

257 DIAVAVLCLKGPRMLVETAQERNETLPALITY-----SATWMLVWV--- 297
 190 DIVAVLAPGSPKLVLVELASSRDEEL_PANVYARPTVSSGNORNRGSGSIRALVGGGG 248

298 MEGDPEAQ-----RVRKNSKAESTERESQDTVAEND_GPSSEWEAQRDHSIG 349
 249 SDGSVVELQAVRNHDVNLQGRNENHMDMVAIRD_IDNVDGIGNGRGGLERSPLV 307

350 P-----HRTPEPESRAVQISSLIA-----GEDPE-----RG 378

Db 92 DSVKEKGMSLGMISLGMALVWLMCUCWVUMLTIVYKPYKVKLIGHLWLSFLFLFTIYV 151
 QY 183 GEVFKTYNAVDVITVALLIWFNGVGMISIHWKGPRQQLQYLMISALMAVLYKYL 242
 Db 152 QEVLKSFDVPSALLVFLPGLGNYGULGMCMCITHKGKGLRQLQYLMISALMAVLYKYL 211
 QY 243 EWTAWLILAVIATSYDVLAVLCLKGPRMLVETAQERNETLPALITYSSTMWV--LYNMA 299
 Db 212 EWTWVFVLFVISWDLVAVLTPKGPRLYVETAQERNEPFPLAIVYVYVWLTAV 271
 QY 300 EGDPEPAGRRVSKS-----KHNAASTERRSQDTVAENDDGFS 337
 Db 272 ENTTDPREPTSSDSNTSTAFFGEASCSETPKPKVRIPOVQVINSNTTASTQNSGVR 331
 QY 338 ESEWEAQRDSHLGHRSIPESRAVQELSSSILAGEDEBERGKLGDFIYVNGKAS 397
 Db 332 VE-----RELAERPTVODAN--FHRHEBERGVKGJGDFIYVNGKAS 376
 QY 398 ATASGDWNTTIAFPVAILGLCJTLIAIFKCALPALPISITPGLUVYP 447
 Db 377 SYF--DWNTTIACTVAILGLCFTLVLLAVFKALPALQFPRFSPDSFTP 424

RESULT 14
 T00724
 presenilin homolog F22013.19 - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
 C;Accession: T00724
 R;Shin, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Colognesi, A.; Ecker, J.R.; submitted to the EMBL Data Library, April 1998
 A;Description: Genomic sequence for *Arabidopsis thaliana* BAC F22013.
 A;Reference number: Z14200
 A;Accession: T00724
 A;Stratoc: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-453 <SHT>
 A;Cross-references: EMBL:AC003981; NRD:93063439; PID:93063457; GSPDB:GN00059; ATSP:F22013
 A;Experimental source: cultivar Columbia
 C;Genetics:
 A;Gene: ATSP:F22013.19
 A;Map position: 1
 A;Introns: 1081
 C;Superfamily: presenilin

Query Match 22.6%; Score 539.5; DB 2; Length 453; Best Local Similarity 33.0%; Pred: No. 2; 3e-34; Mismatches 145; Conservative 19; Indels 71; Gaps 14; Matches 131

82 VMLFVPUVTCMWWVWATIKSVSEYTRKQGQ-LIYTPFEDT 137
 13 IGMWAPVSIWCMFLVWLTYSLSVSDPQIRSAANLIVENPSDSTV--KLEGSLNAT 70

138 IMISVIVMILWVLYKRCYKVIHAWLISLUFFSSPIYLGEVKTYNAVDY 197
 71 VFWVLLIAVFTVILPFLYVYFTNPLKHYMFSAFLVGLGAGFLSIIQHFSIYVDSIT 130

198 VALLIWFNGVGMISIHWKG_PLRQQLQYLMISALMAVLYKYLPEWPAWLLAVIY 256
 131 CFTLLEPNFTTGTLSLVPAGGIPVIRQCYKVMGIVVAAWFTK_LPEWTFWFLVALY 189

257 DIAVAVLCLKGPRMLVETAQERNETLPALITY-----SATWMLVWV--- 297
 190 DIVAVLAPGSPKLVLVELASSRDEEL_PANVYARPTVSSGNORNRGSGSIRALVGGGG 248

298 MEGDPEAQ-----RVRKNSKAESTERESQDTVAEND_GPSSEWEAQRDHSIG 349
 249 SDGSVVELQAVRNHDVNLQGRNENHMDMVAIRD_IDNVDGIGNGRGGLERSPLV 307

350 P-----HRTPEPESRAVQISSLIA-----GEDPE-----RG 378

Db 92 DSVKEKGMSLGMISLGMALVWLMCUCWVUMLTIVYKPYKVKLIGHLWLSFLFLFTIYV 151
 QY 183 GEVFKTYNAVDVITVALLIWFNGVGMISIHWKGPRQQLQYLMISALMAVLYKYL 242
 Db 152 QEVLKSFDVPSALLVFLPGLGNYGULGMCMCITHKGKGLRQLQYLMISALMAVLYKYL 211
 QY 243 EWTAWLILAVIATSYDVLAVLCLKGPRMLVETAQERNETLPALITYSSTMWV--LYNMA 299
 Db 212 EWTWVFVLFVISWDLVAVLTPKGPRLYVETAQERNEPFPLAIVYVYVWLTAV 271
 QY 300 EGDPEPAGRRVSKS-----KHNAASTERRSQDTVAENDDGFS 337
 Db 272 ENTTDPREPTSSDSNTSTAFFGEASCSETPKPKVRIPOVQVINSNTTASTQNSGVR 331
 QY 338 ESEWEAQRDSHLGHRSIPESRAVQELSSSILAGEDEBERGKLGDFIYVNGKAS 397
 Db 332 VE-----RELAERPTVODAN--FHRHEBERGVKGJGDFIYVNGKAS 376
 QY 398 ATASGDWNTTIAFPVAILGLCJTLIAIFKCALPALPISITPGLUVYP 447
 Db 377 SYF--DWNTTIACTVAILGLCFTLVLLAVFKALPALQFPRFSPDSFTP 424

Scoring table: BIOSUM62							Alignments						
Gapop 10.0 , Gapext 0.5							PT13_ARATH						
Searched: 141681 seqs, 52070155 residues							Q16983 <i>acheta dome</i>						
Total number of hits satisfying chosen parameters: 141681							P25162 <i>drosophila</i>						
Minimum DB seq length: 0							P23482 <i>escherichia</i>						
Maximum DB seq length: 200000000							P26365 <i>equulus aca</i>						
Post-processing: Minimum Match 0%							Q19429 <i>rattus norv</i>						
Maximum Match 100%							Q9YR2 <i>rattus norv</i>						
Listing first 45 summaries							Q96040 <i>caenorhabdi</i>						
Database : SwissProt_42:*							Q9J187 <i>mus musculu</i>						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							P52380 <i>human herpe</i>						
SUMMARIES							Q10398 <i>mycobacteri</i>						
RESULT 1							P36028 <i>saccharomy</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q8P18 <i>arabidopsis</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q16983 <i>acheta dome</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P25162 <i>drosophila</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P23482 <i>escherichia</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P26365 <i>equulus aca</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q19429 <i>rattus norv</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q9YR2 <i>rattus norv</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q96040 <i>caenorhabdi</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q9J187 <i>mus musculu</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P52380 <i>human herpe</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q10398 <i>mycobacteri</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P36028 <i>saccharomy</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q8P18 <i>arabidopsis</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q16983 <i>acheta dome</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P25162 <i>drosophila</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P23482 <i>escherichia</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P26365 <i>equulus aca</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q19429 <i>rattus norv</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q9YR2 <i>rattus norv</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q96040 <i>caenorhabdi</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q9J187 <i>mus musculu</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P52380 <i>human herpe</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q10398 <i>mycobacteri</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P36028 <i>saccharomy</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q8P18 <i>arabidopsis</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q16983 <i>acheta dome</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P25162 <i>drosophila</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P23482 <i>escherichia</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P26365 <i>equulus aca</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q19429 <i>rattus norv</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q9YR2 <i>rattus norv</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q96040 <i>caenorhabdi</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q9J187 <i>mus musculu</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P52380 <i>human herpe</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q10398 <i>mycobacteri</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P36028 <i>saccharomy</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q8P18 <i>arabidopsis</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q16983 <i>acheta dome</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P25162 <i>drosophila</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P23482 <i>escherichia</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P26365 <i>equulus aca</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q19429 <i>rattus norv</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q9YR2 <i>rattus norv</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q96040 <i>caenorhabdi</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q9J187 <i>mus musculu</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P52380 <i>human herpe</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q10398 <i>mycobacteri</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P36028 <i>saccharomy</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q8P18 <i>arabidopsis</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q16983 <i>acheta dome</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P25162 <i>drosophila</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P23482 <i>escherichia</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							P26365 <i>equulus aca</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q19429 <i>rattus norv</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q9YR2 <i>rattus norv</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q96040 <i>caenorhabdi</i>						
PSNL_HUMAN STANDARD PRT; 467 AA.							Q9J187 <i>mus musculu</i>						

RT presenilin 1 in the absence of endoproteolysis.";

RA Pelletier E., Vico V., Anthouard V., Bowen L., Madan A., Oin S., Sun H., Du H., Pepin K., Artiguenave F., Robert C., Cruaud C., Bruebs T., Jallion O., Friedlander L., Samion G., Brottier P., Cure S., Segurens B., Aniere F., Samain S., Crespeau H., Abbasi N., Alach N., Boscos D., Dickhoff R., Dors M., Dubois I., Friedland C., Gourvennec M., James R., Madan A., Manley-Bstrada B., Mangenot S., Martins N., Menard M., Oztas S., Ratcliffe A., Shaffer T., Trask B., Vacherie B., Belleneuve C., Belser C., Bresnard-Gonnet M., Bartol-Mavel D., Butard M., Briez-Sil S., Combette S., Dufose-Laurent V., Ferron C., Lechaplais C., Louesse C., Mussellet D., Magdelenat G., Patteau E., Petit E., Sirvain-Trukniewicz E., Vega-Czarny N., Bataille E., Bluet E., Bordelais I., Dubois M., Dumont C., Guerin T., Haffray S., Hammadi R., Muanga J., Pellequin V., Robert D., Wunderle E., Gauguet G., Roy A., Sainte-Marthe L., Verdin J., Verdier-Discalca C., Hillier L.W., Fulton L., McPherson J., Matsuda F., Wilson R., Scalpelli C., Gajay G., Wincker P., Saurin W., Quettier F., Waterston R., Hood L., Weissbach J., "The DNA sequence and analysis of human chromosome 14.";

RT Nature 421:601-607 (2003).

RL [7]

SEQUENCE FROM N.A. (ISOFORM 2).

RP TISSUE-SKIN:

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G., Klausner R.D., Collins F.S., Wagner L., Sheeney C.M., Schuller G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Brat N.K., Hopkins R.F., Jordan H., Moote T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bernaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquai-Lambo N.E., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., Mcowan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W., Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fabej J., Helton E., Kettlerman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmitz J., Myers R.M., Butterfield I.S.N., Krywinski M.I., Skalska U., Smailus D.E., Schenck A., Schein J.E., Jocic S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL [8]

SEQUENCE OF 1-113 FROM N.A.

RA Tsujimura A., Hashimoto-Gotoh T.; submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

RL [9]

SEQUENCE OF 1-113 FROM N.A.

RA SUBCELLULAR LOCATION AND TISSUE SPECIFICITY.

RP MEDLINE=96160372; PubMed=8574969;

RA Kovacs D.M., Faustet H.J., Page K.J., Kim T.-W., Moir R.D., Merriam D.E., Hollister R.D., Hallmark O.G., Mancini R., Felsenstein K.M., Hyman B.T., Tanzi R.E., Wasco W.; "Alzheimer-associated presenilins 1 and 2: neuronal expression in brain and localization to intracellular membranes in mammalian cells"; "Neurology 55:224-229 (1996)."

RL [10]

PROCESSING.

RP MEDLINE=97317150; PubMed=9173929;

RA Podlioni M.B., Citron M., Amaraante P., Sherrington R., Xia W., Zhang J., Diehl T., Levesque G., Fraser P., Haass C., Koo B.H., Seubert P., St. George-Hyslop P., Teplow D.B., Selkoe D.J.; "Presenilin proteins undergo heterogeneous endoproteolysis between Thr291 and Ala299 and occur as stable N- and C-terminal fragments in normal and Alzheimer brain tissue.";

RL [11]

FUNCTION, AND MUTAGENESIS OF MET-292.

RP MEDLINE=20014554; PubMed=10545183;

RA Steiner H., Romig H., Pesold B., Philipp U., Baader M., Citron M., Loetscher H., Jacobsen H., Haass C.; "Amyloidogenic function of the Alzheimer's disease-associated

RT presenilin 1 in the absence of endoproteolysis.";

RL Biochemistry 38:14600-14605(1999).

RA [12]

FUNCTION.

RP MEDLINE=20062913; PubMed=10593990;

RA Ray W.J., Yao M., Mumm J., Schroer E.H., Saftig P., Wolfe M., Seikoe D.J., Kopp R., Goate A.M.; "Cell surface presenilin-1 participates in the gamma-secretase-like proteolysis of Notch.";

RT J. Biol. Chem. 274:36801-36807(1999).

RL [13]

FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.

RP MEDLINE=99221465; PubMed=10206644;

RA Wolfe M.S., Xia W., Ostaszewski B.L., Diehl T.S., Kimberly W.T., Selkoe D.J.; "Two transmembrane aspartates in presenilin-1 required for presenilin endoproteolysis and gamma-secretase activity.";

RL Nature 398:513-517(1999).

RA [14]

FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.

RP MEDLINE=20359435; PubMed=1089933;

RA Berezowska O., Jack C., McLean P., Aster J.C., Hicks C., Xia W., Wolfe M.S., Kimberly W.T., Weinmaster G., Selkoe D.J., Hyman B.T.; "Aspartate mutations in presenilin and gamma-secretase inhibitors both impair notch1 proteolysis and nuclear translocation with relative preservation of notch1 signaling.";

RT J. Neurochem. 75:583-593(2000).

RL [15]

FUNCTION, AND MUTAGENESIS OF LEU-286.

RP MEDLINE=2028925; PubMed=10811883;

RA Klicic L., Walter J., Miltzau D.B., Teplow D.B., Baumeister R., Romig H., Capell A., Steiner H., Haass C.; "Separation of presenilin function in amyloid beta-peptide generation and endoproteolysis of Notch.";

RT Proc. Natl. Acad. Sci. U.S.A. 97:5913-5918(2000).

RL [16]

FUNCTION.

RP MEDLINE=1236248; PubMed=9437013;

RA Baksi L., Marambadi P., Eftimioopoulos S., Georgakopoulos A., Wen P., Cui W., Shioi J., Koo E., Ozawa M., Friedrich V.L., Robakis N.K.; "Presenilin-1 binds cytoplasmic epithelial cadherin, inhibits cadherin/p120 association, and regulates stability and function of the catenin/catenin adhesion complex.";

RT Proc. Natl. Acad. Sci. U.S.A. 98:2381-2386 (2001).

RL [17]

INTERACTIONS WITH FILM AND FILB.

RP MEDLINE=9899890; PubMed=9437013;

RA Zhang W., Han S.W., McKeel D.W., Goate A., Wu J.Y.; "Interaction of presenilins with the filamin family of actin-binding proteins.";

RT J. Neurosci. 18:914-922(1998).

RL [18]

INTERACTION WITH DELTA-2 CATEPININ.

RP MEDLINE=99155075; PubMed=10034741;

RA Levesque G., Yu G., Nishimura M., Zhang D.M., Levesque L., Yu H., Xu D., Liang Y., Roseava E., Ikeda M., Duthie M., Murgolo N., Wang L., Vandevertre P., Bayne M.L., Strader C.D., Rommens J.M., Fraser P.B., St. George-Hyslop P.; "Presenilins interact with armadillo proteins including neural-specific plakophilin-related protein and beta-catenin.";

RT J. Neurochem. 72:999-1008(1999).

RL [19]

INTERACTION WITH HERPUD1.

RP MEDLINE=21395327; PubMed=11799129;

RA Saito K., Kawamura T., Kokame K., Yamaguchi H., Shiraishi H., Suzuki R., Suzuki T., Kawachi M., Miyata T., Kitamura T., De Strooper B., Yanagisawa K., Komano H.; "Endoplasmic reticulum stress-inducible protein, Herp, enhances presenilin-mediated generation of amyloid beta-protein.";

RT J. Biol. Chem. 277:12915-12920(2002).

RL [20]

COMPONENT OF A GAMMA-SECRETASE COMPLEX WITH PEN2; PSEN1/PSEN2 AND NESTIN.

Query Match 99.5%; Score 2378; DB 1; Length 467;
 Best Local Similarity 99.6%; Pred. No. 3.1e-156; Indels 0; Gaps 0;
 Matches 465; Conservative 1; Mismatches 1; Del 0; Insert 0;

Qy 1 MTELPPAPLSTFQNAQOMSBDNHLNSNTRSQNDRERQHNDRSLGHPEPLNSGRPQNSR 60
 Db 1 MTELPPAPLSTFQNAQOMSBDNHLNSNTRSQNDRERQHNDRSLGHPEPLNSGRPQNSR 60

Qy 61 QVVEQDEDEDEELTLKGAKHVKIMFPUVTCMVWVATIKSVSFYTRDGQLIYPTPE 120
 Db 61 QVVEQDEDEDEELTLKGAKHVKIMFPUVTCMVWVATIKSVSFYTRDGQLIYPTPE 120

Qy 121 DTEVQGRALHSNAAIMISIVMVTILLWVLYKRCYKTHAWLISLILLFFPSFI 180
 Db 121 DTEVQGRALHSNAAIMISIVMVTILLWVLYKRCYKTHAWLISLILLFFPSFI 180

Qy 181 YLGEVFKTYNAVDYITVALLWVLYKRCYKTHAWLISLILLFFPSFI 240
 Db 181 YLGEVFKTYNAVDYITVALLWVLYKRCYKTHAWLISLILLFFPSFI 240

Qy 241 LPETWTLILAVISVYDVAVLCKPLRMLVETQERNETLPALYSSM 300
 Db 241 LPETWTLILAVISVYDVAVLCKPLRMLVETQERNETLPALYSSM 300

Db 241 LPETWTLILAVISVYDVAVLCKPLRMLVETQERNETLPALYSSM 300

Qy 301 GDEPAAQRVSKNSKNAESTERESDQTVAENDGGFSEWEAQDRSHLGHPEPLNSGRPQNSR 360
 Db 301 GDEPAAQRVSKNSKNAESTERESDQTVAENDGGFSEWEAQDRSHLGHPEPLNSGRPQNSR 360

Qy 361 VQELSSILAGEDPEERGVKLGLGDFIYFYSVLUKGASATASGDWNTTACFVAILIGCL 420
 Db 361 VQELSSILAGEDPEERGVKLGLGDFIYFYSVLUKGASATASGDWNTTACFVAILIGCL 420

Qy 421 TMLLAIFKKGALPAUTISITGLVVFATDYLQWQFMDQIAFHQYI 467
 Db 421 TMLLAIFKKGALPAUTISITGLVVFATDYLQWQFMDQIAFHQYI 467

RESULT 2

PSNL_MACFA ID PSNL_MACFA STANDARD PRT; 467 AA.

AC 08HXR; DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE PRESENILIN 1 (PS-1).

GN PSNL OR PSLN OR PS1.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Brukaryota; Metazoa; Chordata; Craniata; Bilateria; Euteleostomi;
 OC Mammalia; Buteraria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 NCBI_TAXID=9541; [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Frontal cortex;
 RA Kubota, J., Osada, N., Hida, M., Sugano, S., Hashimoto, K.;
 RT "Isolation and characterization of cDNA for macaque neurological
 disease genes.",
 Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

-I- FUNCTION: Probable catalytic subunit of the gamma-secretase complex, an endoprotease complex that catalyzes the intramembrane cleavage of integral membrane proteins such as Notch receptors and APP (beta-amyloid precursor protein). Requires the other members of the gamma-secretase complex to have a protease activity. May play a role in intracellular signaling and gene expression or in linking chromatin to the nuclear membrane. Regulates epithelial-mesenchymal transition (By similarity).
 -I- SUBUNIT: Homodimer. Component of a presenilin homodimer (PSNL or PSEN2), complex composed of a presenilin homodimer (PSNL or PSEN2), presenilin 1 (PS-1) and APP (beta-amyloid precursor protein). Such minimal complex is sufficient for secretase activity, although other components may exist. Predominantly heterodimer of a N-terminal (NTP) and a C-terminal (CTF) endoproteolytical fragment.

CC Associates with proteolytic processed C-terminal fragments C83 and C99 of the amyloid precursor protein (APP). Associates with NOTCH1. Binds to cadherin 1, beta-catenin, delta-2 catenin and plakophilin 4. Interacts with DCK3. Interacts with HERNDL, FLNA and F1NB (By similarity).

CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and endoplasmic reticulum (By similarity).

CC -I- PTM: Phosphorylated on serine residues (By similarity).

CC -I- SIMILARITY: Belongs to the presenilin family.

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CC EMBL; AB083326; BAC0605.1; -.

CC DR InterPro; IPR00639; Peptidase_A22.

CC DR InterPro; IPR00108; Peptidase_A22A.

CC DR Pfam; PF01080; Presenilin_1.

CC DR PRINTS; PRO1072; PRESENILIN.

DR SMART; S000730; PSN_1.

KW Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.

FT CHAIN 1 PRESENILIN 1 NTP SUBUNIT (BY SIMILARITY).

FT CHIN 298 PRESENILIN 1 CTF SUBUNIT (BY SIMILARITY).

FT TRANSM 83 103 PRESENTILIN.

FT TRANSM 133 153 PRESENTILIN.

FT TRANSM 159 179 PRESENTILIN.

FT TRANSM 191 211 PRESENTILIN.

FT TRANSM 221 241 PRESENTILIN.

FT TRANSM 244 264 PRESENTILIN.

FT TRANSM 408 428 PRESENTILIN.

FT TRANSM 433 453 PRESENTILIN.

FT SITE 291 292 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY SIMILARITY).

FT SITE 292 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY SIMILARITY).

FT SEQUENCE 467 AA; 52573 MW; 0D5EABD73BE30F3 CRC64;

SO Query Match 98.5%; Score 2354; DB 1; Length 467;
 Best local Similarity 98.5%; Pred. No. 1.5e-156; Indels 0; Gaps 0;
 Matches 462; Conservative 1; Mismatches 4; Del 0; Insert 0;

Qy 1 MTELPPAPLSTFQNAQOMSBDNHLNSNTRSQNDRERQHNDRSLGHPEPLNSGRPQNSR 60
 Db 1 MTELPPAPLSTFQNAQOMSBDNHLNSNTRSQNDRERQHNDRSLGHPEPLNSGRPQNSR 60

Qy 61 QVVEQDEDEDEELTLKGAKHVKIMFPUVTCMVWVATIKSVSFYTRDGQLIYPTPE 120
 Db 61 QVVEQDEDEDEELTLKGAKHVKIMFPUVTCMVWVATIKSVSFYTRDGQLIYPTPE 120

Qy 121 DTEVQGRALHSNAAIMISIVMVTILLWVLYKRCYKTHAWLISLILLFFPSFI 180
 Db 121 DTEVQGRALHSNAAIMISIVMVTILLWVLYKRCYKTHAWLISLILLFFPSFI 180

Qy 181 YLGEVFKTYNAVDYITVALLWVLYKRCYKTHAWLISLILLFFPSFI 240
 Db 181 YLGEVFKTYNAVDYITVALLWVLYKRCYKTHAWLISLILLFFPSFI 240

Qy 241 LPETWTLILAVISVYDVAVLCKPLRMLVETQERNETLPALYSSM 300
 Db 241 LPETWTLILAVISVYDVAVLCKPLRMLVETQERNETLPALYSSM 300

Qy 301 GDEPAAQRVSKNSKNAESTERESDQTVAENDGGFSEWEAQDRSHLGHPEPLNSGRPQNSR 360
 Db 301 GDEPAAQRVSKNSKNAESTERESDQTVAENDGGFSEWEAQDRSHLGHPEPLNSGRPQNSR 360

Qy 361 VQELSSILAGEDPEERGVKLGLGDFIYFYSVLUKGASATASGDWNTTACFVAILIGCL 420
 Db 361 VQELSSILAGEDPEERGVKLGLGDFIYFYSVLUKGASATASGDWNTTACFVAILIGCL 420

DR	Db	RESULT 3
PSNL-MICMU	PSNL-MICMU	STANDARD; PRT; 467 AA.
ID	PSNL-MICMU	
AC	P79802;	
DT	15-JUL-1999 (Rel. 38, Created)	
DT	15-JUL-1999 (Rel. 38, Last sequence update)	
DT	15-MAR-2004 (Rel. 43, Last annotation update)	
DE	presenilin 1 (PS-1)	
GN	PSEN1 OR PSNL OR PSL.	
OS	Microcebus murinus (lesser mouse lemur)	
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butcheria; Primates; Strepsirrhini; Cheirogaleidae; Microcebus.	
OC	Microcebus.	
OC	NCBI TaxID:30608;	
RN	[1] - Sequence from N. A. (ISOFORMS I-463 AND I-467).	
RC	SEQUENCE-Brain;	
RX	Medline=97079199; Pubmed=8920931;	
RA	Calenda A., Mestre-Francés N., Czech C., Pradier L., Bons N., Belli M.;	
RT	"Molecular cloning, sequencing, and brain expression of the presenilin 1 gene in Microcebus murinus", Biochem. Biophys. Res. Commun. 228:430-439 (1996).	
RL		
CC	-!- FUNCTION: Probable catalytic subunit of the gamma-secretase complex, an endoprotease complex that catalyzes the intramembrane cleavage of integral membrane proteins such as Notch receptors and APP (beta-amyloid precursor protein). Requires the other members of the gamma-secretase complex to have a protease activity. May play a role in intracellular signaling and gene expression or in linking chromatin to the nuclear membrane. Regulates epithelial-mesenchymal transition.	
CC	-!- SUBUNIT: Homodimer. Component of the gamma-secretase complex composed of a presenilin homodimer (PSEN1 or PSEN2), nicastrin (NCSTN), APH1A (APH1A or APH1B) and PEN2. Such minimal complex is sufficient for secretase activity, although other components may exist. Predominantly heterodimer of a N-terminal (NPF) and a C-terminal (CTF) endoproteolytic fragment.	
CC	-!- ASSOCIATION: Associates with C99, the amyloid precursor protein (APP). Associates with NOTCH1. Binds to cadherin 1, beta-catenin, delta-2-catenin and plakophilin 4. Interacts with DCK3. Interacts with HERCUD1, FNAA and FINB (By similarity).	
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and endoplasmic reticulum (By similarity).	
CC	-!- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2; Name=I-467; IsoIa=P79802-1; Sequence=Displayed;	
CC	Name=I-463; IsoIa=P79802-2; Sequence=VSP_005193; IsoIa=P79802-2; Sequence=VSP_005193;	
CC	-!- TISSUE SPECIFICITY: Found predominantly in neurons of the different cortical layers and hippocampus but also in subcortical structures.	
CC	-!- PTM: Phosphorylated on serine residues (By similarity).	
CC	-!- SIMILARITY: Belongs to the presenilin family.	
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DR	EMBL; Z71333; CA095930.1; -.	
DR	PIR; JC5080; JC5080.	
DR	PIR; JC5081; JC5081.	
DR	MEROPS; A22_001; -.	
DR		
DR	RESULT 4	
PSNL-MOUSE	PSNL-MOUSE	STANDARD; PRT; 467 AA.
ID	PSNL-MOUSE	
AC	P49769; Q91WKG; Q9JLP9;	

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Presenilin 1 (PS-1) (S182 protein).
 GN PSEN1 OR PSNL1 OR ADDH.
 OS Mus musculus (Mouse).
 OC Bokaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A. (ISOFORM 1).
 RT TISSUE=Brain;
 RX MEDLINE=95319502; PubMed=7596406;
 RX Sherrington R., Rogaev E.I., Liang Y., Rogaeva E.A., Levesque G.,
 RA Ikeda M., Chi H., Lin C., Li G., Holman K., Tsuda T., Mar L.,
 RA Focini J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rinero I.,
 RA Pinesi L., Nee L., Chumakov I., Pollen D., Brookes A.,
 RA Samaneu P., Polinsky R.J., Wasco W., da Silva H.A.R., Haines J.L.,
 RA Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E.,
 RA Rommens J.M., St George-Hyslop P.H.;
 RT "Cloning of a gene bearing missense mutations in early-onset familial
 Alzheimer's disease";
 RN Nature 375:754-760(1995).
 RN [2] SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=29/SvJ;
 RX MEDLINE=9295283;
 RA Mittuda N., Roses A.D., Vitek M.P.,
 RT "Transcriptional regulation of the mouse presenilin-1 gene.;"
 RL J. Biol. Chem. 272:23483-23497(1997).
 RN [3] SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=SAM P8; TISSUE=Hippocampus;
 RA Kumar V.B., Vyas K.C., Choudhary V., Franko M., Flood J.F.,
 RA Morley J.E.;
 RT "Molecular cloning and tissue distribution of presenilin-1 in
 senescence accelerated mice (SAM P8) mice.;"
 RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [4] SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=FB/BN; TISSUE=Eye, Liver, and Retina;
 RX MEDLINE=97442406; PubMed=12477932;
 RA Strauborg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klaunser R.D., Collins F.S., Wagner L., Sharnmen C.M., Schuler G.D.,
 RA Aletschul S.F., Zeeberg B., Buetow K.H., Bhat N.K.,
 RA Hopkin R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Loqueland N.A., Peters G.J., Abramson R.D., Mullally S.J.,
 RA Raha S.S., Lequerre S., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fainey J., Heitton E., Kettman M., Maden A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
 RA Butterfield Y.S.N., Krywienski M.I., Skalicka U., Smailus D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5] INTERACTION WITH DOCK3.
 RC TISSUE=brain;
 RX MEDLINE=20312861; PubMed=10854253;
 RA Kashiba A., Ioshida H., Lee S., Paladino T., Liu Y., Chen Q.,
 RA Dargusch R., Schubert D., Kimura H.,
 RT "Isolation and characterization of novel presenilin binding
 protein.;"
 RT "Protein.;"
 RA J. Neurochem. 75:109-115(2000)
 CC -!- FUNCTION: Probable catalytic subunit of the gamma-secretase
 complex, an endoprotease complex that catalyzes the intramembrane

cleavage of integral membrane proteins such as Notch receptors and APP (beta-amyloid precursor protein). Requires the other members of the gamma-secretase complex to have a protease activity. May play a role in intracellular signaling and gene expression or in linking chromatin to the nuclear membrane. Regulates epithelial-mesenchymal transition (EMT) and a C-terminal (CTP) endoproteolytical fragment.
 CC SUBUNIT: Homodimer. Component of the gamma-secretase complex, a complex composed of a presenilin homodimer (PSEN1 or PSEN2), nicastrin (NCSTN), APH1 (APHL or APH1B) and PEN2. Such minimal complex is sufficient for Secretase activity, although other components may exist. Predominantly heterodimer of a N-terminal (NTF) and a C-terminal (CTP) endoproteolytical fragment.
 CC ASSOCIATES WITH: Proteolytic processed C-terminal fragments C83 and C99 of the amyloid precursor protein (APP). Associates with NOTCH1. Binds to cadherin 1, beta-catenin, delta-2 catenin and plakophilin 4. Interacts with DOCK3. Interacts with HERRUD1, FLNA and FLNB (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and endoplasmic reticulum (BY SIMILARITY).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P49769-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P49769-2; Sequence=VSP_008381; VSP_008382;
 CC Note=Due to intron retention. No experimental confirmation
 CC available;
 CC -!- PTM: Phosphorylated on serine residues (BY SIMILARITY).
 CC -!- SIMILARITY: Belongs to the presenilin family.
 CC -----
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 DR EMBL; L2177; AAC42091;
 DR EMBL; AF007560; AAB20491;
 DR EMBL; AF49111; AAF21531;
 DR EMBL; BC00409; AAH04091;
 DR EMBL; BC00409; AAH04091;
 DR PIR; 178388; 178388.
 DR MEROPS; A22.001;
 DR MGD; MGI:1202717; Psen1.
 DR GO; GO:0005783; C: endoplasmic reticulum; IDA.
 DR GO; GO:0016020; C: membrane; IDA.
 DR GO; GO:0005515; P: protein binding; IPI.
 DR InterPro; IPR0066639; Peptidase_A22.
 DR InterPro; IPR001108; Peptidase_A22A.
 DR Pfam; PF01080; Presenilin_1.
 DR PRINTS; PRO1072; PRESENILIN.
 DR SMART; SM00730; PSN_1.
 DR SMART; SM00730; PSN_1.
 KW Transmembrane; Phosphorylation; Endoplasmic reticulum; Goigi stack;
 KW Alternative splicing;
 FT CHAIN 1 298
 FT DOMAIN 299 467
 FT TRANSMEM 1 82
 FT TRANSMEM 83 103
 FT DOMAIN 104 132
 FT TRANSMEM 133 153
 FT DOMAIN 154 160
 FT TRANSMEM 161 181
 FT DOMAIN 182 194
 FT TRANSMEM 195 215
 FT DOMAIN 216 220
 FT TRANSMEM 221 241
 FT DOMAIN 242 243
 FT TRANSMEM 244 264
 FT DOMAIN 265 407
 FT TRANSMEM 408 428
 FT TRANSMEM 433 453

FT	SITE	291	292	ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY SIMILARITY).	RN	[2]
FT	SITE	292	293	ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY SIMILARITY).	RP	SEQUENCE FROM N.A.
FT	VARSPLIC	257	261	DIVISION 2 (IN isoform 2).	RC	TISSUE=Brain;
FT	VARSPLIC	262	467	/Pfam=VSP_008381. Missing (In isoform 2). /Pfam=VSP_008382.	STRAIN=Mouse;	
FT	VARIANT	9	9	S -> T (IN STRAIN SAM P8).	RC	STRAIN=Star;
FT	VARIANT	40	40	D -> E (IN STRAIN SAM P8).	RC	STRAIN=Star;
FT	VARIANT	67	67	E -> V (IN STRAIN SAM P8).	RC	STRAIN=Star;
FT	VARIANT	196	195	CW (IN STRAIN SAM P8).	RA	MedlineID=625262; PubMed=810164;
FT	VARIANT	321	322	ER -> RRD (IN STRAIN SAM P8).	RA	RAKUHASHI H., MURAYAMA M., TAKAHASHIMA A., MERCKEN M., NAKAZATO Y., NOGUCHI K., IMABORI K.,
SQ	SEQUENCE	467	AA:	52639 MW; D07215B4BAD2D549 CRC64;	RA	"Molecular cloning and expression of the rat homologue of presenilin-1";
Query Match 93.2%; Score 2228; DB 1; Length 467;						
Best Local Similarity 92.3%; Prod. No. 8.4e-18; Matches 431; Conservative 19; Mismatches 17; Indels 0; Gaps 0;						
QY	1	MTELPAPLISVQNAQMSDNLHSNTVRSONDNERQHENDRSLIGHBPLSNRPGQNSR	60	/Pfam=VSP_008380.	RA	Neurosci. Lett.; 206:113-116(1996).
Db	1	MTELPAPLISVQNAQMSDNLHSNTVRSONDNERQHENDRSLIGHBPLSNRPGQNSR	60	/Pfam=VSP_008380.	RA	-I- FUNCTION: Probable catalytic subunit of the gamma-secretase complex, an endoprotease complex that catalyzes the intramembrane cleavage of integral membrane proteins such as Notch receptors and APP (beta-amyloid precursor protein). Requires the other members of the gamma-secretase complex to have a protease activity. May play a role in intracellular signaling and gene expression or in linking chromatin to the nuclear membrane. Regulates epithelial-cadherin function (By similarity).
QY	61	QVVAQDEEDEBELLTKYKGRHVMLFVPTLCWVVAATKSYSPYRKKDQJLIVPFT	120	/Pfam=VSP_008380.	CC	-I- SUBUNIT: Homodimer. Component of the gamma-secretase complex, a complex composed of a presenilin homodimer (PSEN1 or PSEN2), nicatinin (NCNP), APH1 (APH1A or APH1B) and PEN2. Such minimal complex is sufficient for secretase activity, although other components may exist. Predominantly heterodimer of a N-terminal (NPF) and a C-terminal (CTF) endoproteolytic fragment.
Db	61	QVVAQDEEDEBELLTKYKGRHVMLFVPTLCWVVAATKSYSPYRKKDQJLIVPFT	120	/Pfam=VSP_008380.	CC	Associates with proteolytic processed C-terminal fragments C83 and C99 of the amyloid precursor protein (APP). Associates with NOTCH1. Binds to cadherin 1, beta-catenin, delta-2 catenin and plakophilin 4. Interacts with DDX3. Interacts with HERPUD1, FLNA, and FNAB (By similarity).
QY	121	DTEEVGQRALHSNTNAAMSVVMTLILVWYKRYKVKHAWLITSLILVFFPSI	180	/Pfam=VSP_008380.	CC	-I- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and endoplasmic reticulum (By similarity).
Db	121	DTEEVGQRALHSNTNAAMSVVMTLILVWYKRYKVKHAWLITSLILVFFPSI	180	/Pfam=VSP_008380.	CC	-I- PTM: Phosphorylated on serine residues (By similarity).
QY	181	YLGIVFKTIVNAVDYITVALLINFGVGWGMISHWKGLRQOAYLIMISALMFIKY	240	/Pfam=VSP_008380.	CC	-I- SIMILARITY: Belongs to the presenilin family.
Db	181	YLGIVFKTIVNAVDYITVALLINFGVGWGMISHWKGLRQOAYLIMISALMFIKY	240	/Pfam=VSP_008380.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
QY	241	LPEVNTMILAVIISVYDVAVTCIGKPRMLVTAQENETLPPALYSSTMVLMVMAE	300	/Pfam=VSP_008380.	CC	-----
Db	241	LPEVNTMILAVIISVYDVAVTCIGKPRMLVTAQENETLPPALYSSTMVLMVMAE	300	/Pfam=VSP_008380.	CC	-----
QY	301	GDPEAQQRSSKNSKNAESTERESQDTVAENDGGSSEWEARDSHGPRSTPESRA	360	/Pfam=VSP_008380.	CC	-----
Db	301	GDPEAQQRSSKNSKNAESTERESQDTVAENDGGSSEWEARDSHGPRSTPESRA	360	/Pfam=VSP_008380.	CC	-----
QY	361	VQEVLSSSILAGGEDDEBBERGVGLGDPFISVLUVKAASITASGDNNTIACVAILIGCL	420	/Pfam=VSP_008380.	DR	EMBL; D82363; BAA1564.1; --.
Db	361	VQEVLSSSILAGGEDDEBBERGVGLGDPFISVLUVKAASITASGDNNTIACVAILIGCL	420	/Pfam=VSP_008380.	DR	EMBOS; A22.01; --.
QY	421	TLLIAIFKFLKALPAPISTTGLVYFATDYLVQPFMDQLAHQFYI	467	/Pfam=VSP_008380.	DR	InterPro; IPR006639; Peptidase_A22A.
Db	421	TLLIAIFKFLKALPAPISTTGLVYFATDYLVQPFMDQLAHQFYI	467	/Pfam=VSP_008380.	DR	Pfam; PF01080; Presenilin; 1.
RESULT 5	PSNL1 RAT	STANDARD;	PRT;	468 AA.	DR	PRINTS; PR01072; PRESENILIN.
ID	PSNL1 RAT				DR	SMART; SW00730; PSN; 1.
AC	P97887;	997529;			DR	KW Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
DT	15-JUL-1993	(Rel. 38, Created)			FT	CHAIN 1 298 PRESENILIN 1 NTP SUBUNIT (BY SIMILARITY).
DT	15-JUL-1999	(Rel. 38, Last sequence update)			FT	DOMAIN 1 97 PRESENILIN 1 CTF SUBUNIT (BY SIMILARITY).
DT	15-MAR-2004	(Rel. 43, Last annotation update)			FT	TRANSMEM 1 97 POTENTIAL.
DE	Presenilin 1 (PS-1) (S182 protein).				FT	TRANSMEM 83 103 POTENTIAL.
GN	PSNL1 OR PSNL1.				FT	TRANSMEM 104 132 LUMINAL POTENTIAL.
OS	Rattus norvegicus (Rat).				FT	TRANSMEM 133 153 LUMINAL POTENTIAL.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				FT	TRANSMEM 154 160 CYTOPLASMIC (POTENTIAL).
OC	Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				FT	TRANSMEM 161 181 POTENTIAL.
OX	NCBI_TaxID=10116;				FT	TRANSMEM 182 194 LUMINAL (POTENTIAL).
RN	[1]				FT	TRANSMEM 195 215 POTENTIAL.
	SEQUENCE FROM N.A.				FT	TRANSMEM 216 220 CYTOPLASMIC (POTENTIAL).
RP	STRAIN=Wistar, TISSUE=Brain;				FT	TRANSMEM 221 241 POTENTIAL.
RC	MEDLINE=7199371; PubMed=9041347;				FT	TRANSMEM 242 243 LUMINAL (POTENTIAL).
RX	Taniguchi T., Hashimoto T., Taniguchi R., Shimada K., Kawamata T.,				FT	TRANSMEM 244 264 POTENTIAL.
RA	Yasuda M., Nakai M., Terasawa A., Koizumi T., Maeda K., Tanaka C.,				FT	TRANSMEM 265 407 CYTOPLASMIC (POTENTIAL).
RT	"Cloning of the cDNA encoding rat presenilin-1.,"				FT	TRANSMEM 408 428 POTENTIAL.
RL	Gene 186:73-75 (1997).				FT	TRANSMEM 433 453 POTENTIAL.
					FT	TRANSMEM 454 473 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY SIMILARITY).
					FT	TRANSMEM 474 493 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY SIMILARITY).
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					FT	TRANSMEM 594 613 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY SIMILARITY).
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					FT	TRANSMEM 2454 2473 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY SIMILARITY).

SQ	SEQUENCE	468 AA;	52790 MW;	17CB791E88A16FC0 CRC64;
Query Match		92.0%;	Score 2200.5;	DB 1; Length 468;
Best Local Similarity		91.9%;	Pred. No. 6.9e-146;	
Matches	431;	Conservative	20;	Mismatches 15; Indels 3; Gaps 3;
QY	1	MTELPAVLPSYQNAQNSEDNHLNSNTVRSQNDRERQHNRRLSRGHPEPLNSGRPGNS	59	CC
Db	1	MTELPAVLPSYQNAQNSEDNHLNSNTVRSQNDRERQHNRRLSRGHPEPLNSGRPGNS	59	CC
QY	60	RQVWQDEDEBELTLYGAKHVLFLVPTLICMVVATIKSVSFYTRKDQQLYTFPT	119	CC
Db	60	RQVWQDEDEBELTLYGAKHVLFLVPTLICMVVATIKSVSFYTRKDQQLYTFPT	119	CC
QY	120	EDTETVQRALHSILNAIMSVIVNTLILVLYKRCYKTHAWLISLILFFPSF	179	CC
Db	120	EDTETVQRALHSILNAIMSVIVNTLILVLYKRCYKTHAWLISLILFFPSF	179	CC
QY	120	EDTETVQRALHSILNAIMSVIVNTLILVLYKRCYKTHAWLISLILFFPSF	179	CC
Db	120	EDTETVQRALHSILNAIMSVIVNTLILVLYKRCYKTHAWLISLILFFPSF	179	CC
QY	180	YLGEVFKTYNAVDITVALLIINFGVGMISIHWKGPLRLQQYLIMISALMVF	239	CC
Db	180	YLGEVFKTYNAVDITVALLIINFGVGMISIHWKGPLRLQQYLIMISALMVF	239	CC
QY	240	YLPENWTLILAVIYDVAVLCLKGPLMLVTAQERNETLPALIYSTMVLNVA	299	CC
Db	240	YLPENWTLILAVIYDVAVLCLKGPLMLVTAQERNETLPALIYSTMVLNVA	299	CC
QY	300	EGDPPEAQRRVSKNSKNESTERESQDTVAENDGGFSEWEAQRDHSILGPHRSTPSR	358	CC
Db	300	EGDPPEAQRRVSKNSKNESTERESQDTVAENDGGFSEWEAQRDHSILGPHRSTPSR	359	CC
QY	359	RAVQELSSSTIAGEDPEERGVLGLGDFTFYSVAVGKASATASDWNNTIACFVAVIIGL	418	CC
Db	360	RAVQELSSSTIAGEDPEERGVLGLGDFTFYSVAVGKASATASDWNNTIACFVAVIIGL	419	CC
QY	419	CITLILIAIKKALALPISITFGLVYFATDYLVQPEMDQLAQPHOFYI	467	CC
Db	420	CITLILIAIKKALALPISITFGLVYFATDYLVQPEMDQLAQPHOFYI	468	CC
RESULT 6				
PSN1_BOVIN	ID	PSN1_BOVIN	STANDARD;	PRT; 478 AA.
AC	Q8XH7;			
DT	16-OCT-2001 (Rel. 40, created)			
DT	16-OCT-2001 (Rel. 40, last sequence update)			
DT	15-MAR-2004 (Rel. 43, last annotation update)			
DE	Presenilin 1 (PSN-1);			
GN	PSN1.			
OS	Bos taurus (Bovine).			
OC	Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OX	Bovidae; Bovinae; Bos.			
NCBI_TaxID=9913;				
[1]				
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Satara N., Shirasawa T., Mori H.;			
RL	"Molecular cloning of bovine presenilin 1 gene.";			
CC	Submitted (DE-1997) to the EMBL/GenBank/DBJ databases.			
-	FUNCTION: Probable catalytic Subunit of the gamma-secretase complex, an endoprotease complex that catalyzes the intramembrane cleavage of integral membrane proteins such as Notch receptors and APP (beta amyloid precursor protein). Requires the other members of the gamma-secretase complex to have a protease activity. May play a role in intracellular signaling and gene expression or in linking chromatin to the nuclear membrane. Regulates epithelial-mesenchymal function. (By similarity).			
CC	-!- SUBUNIT: Homodimer. Component of the gamma-secretase complex composed of a presenilin homodimer (PSN1 or PSN2), nicastrin (NCNP), APH1 (APH1) and PEN2. Such minimal complex is sufficient for secretase activity, although other components may exist. Predominantly heterodimer of a N-terminal (NTE) and a C-terminal (CTF) endoproteolytical fragment.			
QY	91.0%;	Score 2175.5;	DB 1;	Length 478;
Query Match				
Best Local Similarity		89.3%;	Pred. No. 3.9e-144;	
Matches	427;	Conservative	20;	Mismatches 20; Indels 11; Gaps 2;
QY	1	MTELPAVLPSYQNAQNSEDNHLNSNTVRSQNDRERQHNRRLSRGHPEPLNSGRPGNS	59	CC
Db	1	MTELPAVLPSYQNAQNSEDNHLNSNTVRSQNDRERQHNRRLSRGHPEPLNSGRPGNS	60	CC
QY	60	RQVWQDEDEBELTLYGAKHVLFLVPTLICMVVATIKSVSFYTRKDQQLYTFPT	119	CC
Db	61	QDQVEQEEBEDEBELTLYGAKHVLFLVPTLICMVVATIKSVSFYTRKDQQLYTFPT	120	CC
QY	120	EDTETVQRALHSILNAIMSVIVNTLILVLYKRCYKTHAWLISLILFFPSF	179	CC
Db	121	EDTETVQRALHSILNAIMSVIVNTLILVLYKRCYKTHAWLISLILFFPSF	180	CC
QY	180	YLGEVFKTYNAVDITVALLIINFGVGMISIHWKGPLRLQQYLIMISALMVF	239	CC
Db	181	YLGEVFKTYNAVDITVALLIINFGVGMISIHWKGPLRLQQYLIMISALMVF	240	CC
QY	240	YLPENWTLILAVIYDVAVLCLKGPLMLVTAQERNETLPALIYSTMVLNVA	299	CC
Db	241	YLPENWTLILAVIYDVAVLCLKGPLMLVTAQERNETLPALIYSTMVLNVA	300	CC

QY 300 EGPPEAQRRVSKNSKHNAE-----STERESDQTVENDGGESEEWAQRDHSLG 349
 FT TRANSMEM 127 147 POTENTIAL.
 DB 301 EGDPEAQRKVSKNSHNAQRPANSPTTGTSESQDPTVTESDGGSEBWEAQRDHSLG 360
 FT TRANSMEM 161 181 POTENTIAL.
 QY 350 PHSTPESPAQAVELSSILAGDPEEGVKIGLGDFFFYSVLUVKASATSGDMWTTIA 409
 FT TRANSMEM 184 204 POTENTIAL.
 DB 361. PHSTAESRASAVODISSSTASDEPEEGVKIGLGDFFFYSVLUVKASATSGDMWTTIA 420
 FT TRANSMEM 210 230 POTENTIAL.
 QY 410 CFVAILIGLCLTLLATPKALPALPISITGLVFFATDVQPMDFQAFQFYI 467
 FT TRANSMEM 247 267 POTENTIAL.
 DB 421 CFVAILIGLCLTLLATPKALPALPISITGLVFFATDVQPMDFQAFQFYI 478
 FT TRANSMEM 374 394 POTENTIAL.
 FT TRANSMEM 399 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 371 371 SEQUENCE 433 AA; 48301 MW; 71CCB3F6BB9COAP CRC64;

RESULT 7

PSNL_XENLA STANDARD; PRT; 433 AA.

ID PSNL_XENLA STANDARD; PRT; 433 AA.

AC O13976; 15-JUL-1999 (Rel. 38, Created)
 15-JUL-1999 (Rel. 38, last sequence update)
 10-OCT-2003 (Rel. 42, last annotation update)

DE Presenilin alpha.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 Xenopodinae; Xenopus.

OX NCBI_TAXID=8355;

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=97224465; PubMed=9070286;

RA Tsujimura A., Yasojima K., Hashimoto-Gotoh T.;
 "Cloning of Xenopus presenilin-alpha and -beta cDNAs and their
 differential expression in oogenesis and embryogenesis.";

RT Biochem. Biophys. Res. Commun. 231:392-396 (1997).

RL 1. FUNCTION: Probable catalytic subunit of the gamma-secretase
 complex, an endoprotease complex that catalyzes the intramembrane
 cleavage of integral membrane proteins such as Notch receptors (By
 similarity). May play a role in negative regulation of apoptotic
 cascades during oogenesis and embryogenesis, and in
 developmentally matured tissues such as brain tissue.

2. SUBUNIT: Homodimer. Probable component of the gamma-secretase
 complex, a complex composed of a presenilin homodimer (PS-Alpha or
 PS-beta), nicastrin (NCS1), APH1 and PEN2 (Frb220).

3. SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

4. TISSUE SPECIFICITY: Highest expression in ovaries and to a lesser
 extent in testes, intestine, kidney, brain, eye and lung. Weak
 expression in liver and heart. Present in trace amounts in
 skeletal muscle.

5. DEVELOPMENTAL STAGE: Abundant in early stages of oogenesis. The
 expression is rapidly reduced between meiotic maturation and
 fertilization stages.

6. SIMILARITY: Belongs to the presenilin family.

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 or send an email to license@sb-sib.ch).

CC EMBL; D94427; BAA19570.1; -.

DR PIR; JG5390.

DR MEROPS; A22_001; -.

DR InterPro; IPR006639; Peptidase_A22.

DR InterPro; IPR01108; Peptidase_A22A.

DR Pfam; PF01080; Presenilin_1.

DR PRINTS; PR01072; PRESENTILIN.

DR SMART; S000730; PSN_1.

DR Transmembrane Glycoprotein.

FT TRANSMEM 48 68

FT TRANSMEM 99 119 POTENTIAL.

RP SEQUENCE FROM N.A.

RESULT 8

PSNL_BARE STANDARD; PRT; 456 AA.

ID PSNL_BARE STANDARD; PRT; 456 AA.

AC O9W677; 10-OCT-2003 (Rel. 42, Created)
 10-OCT-2003 (Rel. 42, last sequence update)
 10-OCT-2003 (Rel. 42, last annotation update)

DE Presenilin 1 (PS1) (Zf-PS1).

GN PSN1.

OS Brachydanio rerio (zebrafish) (Danio rerio).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 Cyprinidae; Danio.

OC Cyprinidae; Danio.

OX NCBI_TAXID=7955;

RN [1] SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF ASP-374.

RX MEDLINE=9945270; PubMed=1052267;

RA Leimer U., Lun K., Romig H., Walter J., Gruenberg J., Brand M.,
 Haass C.;
 "Zebrafish (Danio rerio) presenilin promotes aberrant amyloid
 beta-peptide production and requires a critical aspartate residue for
 its function in amyloidogenesis.";
 Biochemistry 38:13602-13609(1999).

RL [2] SEQUENCE FROM N.A.

FT TRANSMEM 204 224 POTENTIAL.
 FT TRANSMEM 227 247 POTENTIAL.
 FT TRANSMEM 253 273 POTENTIAL.
 FT TRANSMEM 291 311 POTENTIAL.
 FT TRANSMEM 363 383 POTENTIAL.
 FT TRANSMEM 390 410 POTENTIAL.
 FT TRANSMEM 415 435 POTENTIAL.
 FT CARBOHYD 387 N-LINKED (GLCNAC . .) (POTENTIAL).
 SQ SEQUENCE 449 AA: 50274 MW: 2C2105FC723F2B CRC64; [3]
 Query Match 61.2%; Score 1462.5; DB 1; Length 449;
 Best Local Similarity 64.1%; Prc. No. 1.4e-94; Matches 302; Conservative 47; Mismatches 75; Indels 47; Gaps 7;
 Matches 302; Conservative 47; Mismatches 75; Indels 47; Gaps 7;
 QY 2 TELPAPLSFFQNAQMSEDNHLSNTVRSONDRQHQHRSIGHPRPLSNRPGQ---- 57
 DB 21 SESPLPLSPQDGYQASEGIFTSY-----HRERQPOSTQNN---EDVPIGRTSGDAY 69
 QY 58 NSRQVVEQDEBDEBLTQYAKEVIMFPVPLQMVNVATKSVSFYTRKGQLIYTP 117
 DB 70 NSETIV--ENEELBLTQYAGRTIVMLFPVPLQMVNVATKSVSFYTRKGQLIYTP 126
 QY 118 FTDEDTETGGRALHSILNAAIMSVIVVNTILAVVLYKRYCYKTHAWLISLLIIFP 177
 DB 127 PSEDTTSVGERLINSVNTILAVVLYKRYCYKTHAWLISLLIIFP 186
 QY 178 SFIYVGEVFTYNTNAMDYPTLWNTIWNFGAVGMICHHWKGPLQOQAYLIMISALMVF 237
 DB 187 TYIYVSEFPTYNTNAMDYPTLWNTIWNFGAVGMICHHWKGPLQOQAYLIMISALMVF 246
 QY 238 IYLPWETAVLILAVISVDLVAVLCKPPLMLVETAQERNETLFPAIYXSTMVNLN 297
 DB 247 IYLPWETAVLILAVISVDLVAVLCKPPLMLVETAQERNETLFPAIYXSTMVNLN 306
 QY 298 MAEGPPEAQVRVKSKHMAESTERESQTTAENDGPFSEEAQRSHLGHFRSTPES 357
 DB 307 MAD-SATADGRMNQVOHQHIDRNTPEGANSTV-----ED 338
 DB 339 AAETRQTOQNSLSSDPEERGKVKGQDPIFYSLVNGKASATASGDNTTACPVALLI 398
 DB 417 GICLTULLIAFKKALPALTSITGLVLFVATDLYQPMQDQIAFHOFYI 467
 QY 399 GLCTTULLIAFKKALPALTSITGLVLFVATDLYQPMQDQIAFHOFYI 449
 DB
 RESULT 10
 PSN2_HUMAN STANDARD; PRT; 448 AA.
 ID PSN2_HUMAN STANDARD; PRT; 448 AA.
 AC P49310; Q96P32;
 DT 01-OCT-1996 (Rel. 34. Created)
 DT 01-OCT-1996 (Rel. 34. Last sequence update)
 DT 15-MAR-2004 (Rel. 43. Last annotation update)
 DE Presentin 2 (PSN2) (STM-2) (ES-1) (AD3LP) (AD5).
 DE PSN2 OR PSNL2 OR AD4 OR PS2 OR STM2.
 GN Homo sapiens (Human).
 OC Bivalvia; Metozoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBITaxon=9606;
 RN [1] SEQUENCE FROM N.A., AND VARIANT AD ILE-141.
 RP SEQUENCE FROM N.A., AND VARIANT AD ILE-141.
 RP MEDLINE=9336581; PubMed=7638622;
 RX Levy-Lahad E., Wasco W., Poirier P., Romano D.M., Oshima J.,
 Pettingell W.H., Yu C.-E., Jondro D., Schmidt S.D., Wang K.,
 Crowley A.C., Fu Y.-H., Guenette S.Y., Galas D., Nemens E.,
 Wijmans E.M., Bird T.D., Scheinlenberg G.D., Tanzi R.E.;
 RA [2] "Candidate gene for the chromosome 1 familial Alzheimer's disease locus";
 RT Science 269:973-977(1995).
 RN SEQUENCE FROM N.A., AND VARIANT AD ILE-141 AND VAL-239.
 RC TISSUE=Brain, and Colon;

RP MEDLINE=95379971; PubMed=7651536;
 RA Rogaei E.I., Sherrington R., Rogaeva E.A., Levesque G., Ikeda M.,
 Liang Y., Chi H., Lin C., Holman K., Tsuda T., Mar L., Sorbi S.,
 Nachmias B., Blacettini S., Amaducci L., Chumakov I., Cohen D.,
 Lamfeil L., Fraser P.E., Fraser J.M., St George-Hyslop P.H.,
 RT "Familial Alzheimer's disease in kindreds with missense mutations in a gene on chromosome 1 related to the Alzheimer's disease type 3 gene";
 RT Nature 376:775-778(1995).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=9610229; PubMed=8618867;
 RA Li J., Ma J., Pottier H.;
 RT "Identification and expression analysis of a potential familial Alzheimer disease gene on chromosome 1 related to AD3.;"
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
 RA Phelan M., Farmer A., Rubin G.M., Hong L.,
 RA Altshul S.F., Zeeberg B., Bluetow K.H., Schaeffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heihs F.,
 RA Diatchenko L., Marsilia K., Farmer A.E., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McCawian P.J., McKernan K.J., Malek J.A., Gunnaratin P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villacon D.K., Muzny D.M., Sodergren E.J., Lu Y., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J.J., Schmitz J.J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Smalius D.E.,
 RA Schnech A., Schein J.E., Jones S.J.M., Marra M.A., Smalius D.E.,
 RT "Gene analysis and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [7]
 RP SEQUENCE OF 1-390 MW: 448 AA.
 RA Xu Y., Hu X., Zhou Y., Peng X., Yuan J., Qiang B.,
 RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [8]
 OC SUBCELLULAR LOCATION AND TISSUE SPECIFICITY.
 RP MEDLINE=96160372; PubMed=857969;
 RX Kovacs D.M., Fabretti H.J., Page K.J., Kim T.-W., Moir R.D.,
 RA Merriam D.E., Hollister R.D., Hallmark O.G., Mancini R.,
 RA Felsenstein K.M., Hyman B.T., Tanzi R.E., Wasco W.,
 RT "Alzheimer-associated presenilins 1 and 2: neuronal expression in
 RT brain and localization to intracellular membranes in mammalian
 RT cells";
 RT Nat. Med. 2:224-229(1996).
 RN [9]
 RP INTERACTIONS WITH F11A AND F11B.
 RX MEDLINE=98099802; PubMed=9437013;
 RX Zhang W., Han W., McKeal D.W., Goate A., Wu J.Y.;
 RT "Interaction of presenilins with the filamin family of actin-binding
 Proteins.;"

DT 15-JUL-1999 (Rel. 38, last sequence update)
 DT 15-MAR-2004 (Rel. 43, last annotation update)
 DE Presenilin 2 (PSN2; Fragment).
 GN PSEN2 OR PSNL2 OR PS2.
 OS Microcebus murinus (Lesser mouse lemur).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Cheirogaleidae;
 OC Microcebus.
 OX NCBI_TaxID=3008;
 RN 11]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=9167105; PubMed=10069575;
 RA Calenda A., Mestre-Frances N., Czech C., Pradier L., Petter A.,
 RA Perret M., Bora N., Bellis M.; Czech C., Pradier L., Petter A.,
 RT "Cloning of the presenilin 2 cDNA and its distribution in brain of
 the primate, *Microcebus murinus*: coexpression with betaAPP and Tau
 proteins". *Neurobiol Dis.* 5:323-333 (1998).
 RT -!- FUNCTION: Probable catalytic subunit of the gamma-secretase
 complex, an endoprotease complex that catalyzes the intramembrane
 cleavage of integral membrane proteins such as Notch receptors and
 APP (beta-amyloid precursor protein). Requires the other members
 of the gamma-secretase complex to have a protease activity. May
 play a role in intracellular signaling and gene expression or in
 linking chromatin to the nuclear membrane. May function in the
 cytoplasmic partitioning of proteins (By similarity).
 CC complex composed of a presenilin homodimer (PSEN1 or PSEN2),
 nicastrin (NCSTN), APH1 (APH1A or APH1B) and PEN2. Such minimal
 complex is sufficient for secretase activity, although other
 components may exist. Interacts with DCK3. Interacts with
 HERPUD1, F11A and F11B (By similarity).
 CC SUBCELLULAR LOCATION: Integral membrane protein. Golgi and
 endoplasmic reticulum (By similarity).
 CC -!- PTM: Phosphorylation on serine residues (By similarity).
 CC -!- SIMILARITY: Belongs to the presenilin family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC
 CC EMBL; Y11440; CAA71228.1; -.
 DR MEROPS; A22.002; -.
 DR InterPro; IPR006319; Peptidase_A22.
 DR InterPro; IPR001108; Peptidase_A22a.
 DR Pfam; PF01080; Presenilin_1.
 DR PRINTS; PR01072; PRESENTILIN.
 DR SMART; SM00730; PSN_1.
 KW Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
 FT CHAIN 1 PRESENTILIN 2 NTF SUBUNIT (BY SIMILARITY).
 FT DOMAIN 298 PRESENTILIN 2 CTF SUBUNIT (BY SIMILARITY).
 FT DOMAIN 1 445 PRESENTILIN 2 CTF SUBUNIT (BY SIMILARITY).
 FT DOMAIN 88 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 109 POTENTIAL.
 FT DOMAIN 139 LUMENAL (POTENTIAL).
 FT DOMAIN 160 POTENTIAL.
 FT DOMAIN 167 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 189 LUMENAL (POTENTIAL).
 FT DOMAIN 201 LUMENAL (POTENTIAL).
 FT DOMAIN 222 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 224 POTENTIAL.
 FT DOMAIN 245 LUMENAL (POTENTIAL).
 FT DOMAIN 249 POTENTIAL.
 FT DOMAIN 250 LUMENAL (POTENTIAL).
 FT DOMAIN 272 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 389 POTENTIAL.
 FT DOMAIN 414 POTENTIAL.
 FT NON_TER 445 LUMENAL (POTENTIAL).
 SQ SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Sahara N., Shirasawa T., Mori H.;
 RA "Molecular cloning of bovine presenilin 2 gene";
 RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RL -!- FUNCTION: Probable catalytic subunit of the gamma-secretase
 complex, an endoprotease complex that catalyzes the intramembrane
 cleavage of integral membrane proteins such as Notch receptor and
 APP (beta-amyloid precursor protein). Requires the other members
 of the gamma-secretase complex to have a protease activity. May
 play a role in intracellular signaling and gene expression or in
 linking chromatin to the nuclear membrane. May function in the
 cytoplasmic partitioning of proteins (By similarity).
 CC complex composed of a presenilin homodimer (PSEN1 or PSEN2),
 nicastrin (NCSTN), APH1 (APH1A or APH1B) and PEN2. Such minimal
 complex is sufficient for secretase activity, although other
 components may exist. Interacts with DCK3. Interacts with
 HERPUD1, F11A and F11B (By similarity).
 CC SUBCELLULAR LOCATION: Integral membrane protein. Golgi and

Query Match 60.2%; Score 1440; DB 1; Length 445;
 Best Local Similarity 65.0%; Pred. No. 5e-93; ID 78; Indels 42; Gaps 8;
 Matches 301; Conservative 42; Mismatches 78; Index 42; Gaps 8;

Qy 3 ELPAPLISYFQNAQMSBDNHSNTVRSQNDNRERBHDNR-SLGHPEPLSNGRQNRQ 61
 Qy 24 ESPSPRSCQSGQGPBDGDTAQWRIQDSBEGDPPDRYVSSGVP---GRPG--- 74
 Db 62 WVEQDDEBLTUKYAKAVUMFVPLGCMVUATKVSQYTRKGQLYTPFED 121
 Db 75 -----PERBLTUKYAKAVUMFVPLGCMVUATKVSQYTRKGQLYTPFED 127
 Db 122 TETVGORALHSILNAAIMSVIVWTTLLVLYKURCKVIAHMLISSLULPFSFY 181
 Db 128 TPSVSDLILSVNLTIMSVIYVNTIYVLYKRCYFPIHGLIMSLMILPFTL 187
 Qy 182 LGEVFLKTYNAMVYDYLVLTWNGAVGWCINHKGPMLQAVLIAASALMVFKL 247
 Db 242 PEWTAMILAVISVYDYLVLTCLKPRMLVETQERNSTLFPALIVYSTMWVUNMABG 301
 Db 248 PEWSAWVILGASVYDYLVLTCLPKGPJPRMLVETQERNSTLFPALIVYSTMWVUNMABG 301
 Qy 302 DPEAQQRVSKSKHNESTERESQDQTAENDGAFSEWEAEQARSHLGHRSPESSRAV 361
 Db 308 DPSSQAL--QLIPYPE--MDSVNLSE--PSPVPEVAPLPGYPP----- 349
 Qy 362 QELSSSILAGDPERGKGLGDRIFPSYLVKGASATASGDMNTIAEVAILIGCIT 421
 Db 350 EBL-----EEEEGRVKLGLGDRIFPSYLVKGAAATGSGDMNTIACVAILIGCIT 402
 DE 422 ILLIAFFKKALPALIPISTGUVFFATDYLWQPMQDQAFHQ 464
 Qy 403 LLLAVVFKKAALPAIPISITGUVFVSTDILVLRPFMDTLAYHQ 445
 Db

RESULT 12

PSN2_BOVIN STANDARD; PRT; 449 AA.

ID PSN2_BOVIN
 AC Q9XT94;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Presenilin 2 (PSN2).
 GN PSN2.
 OS Bos taurus (Bovine).
 OC Bovidae; Bovine; Bos.
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 OX NCBI_TaxID=9913;
 RN 11]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Sahara N., Shirasawa T., Mori H.;
 RA "Molecular cloning of bovine presenilin 2 gene";
 RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RL -!- FUNCTION: Probable catalytic subunit of the gamma-secretase
 complex, an endoprotease complex that catalyzes the intramembrane
 cleavage of integral membrane proteins such as Notch receptor and
 APP (beta-amyloid precursor protein). Requires the other members
 of the gamma-secretase complex to have a protease activity. May
 play a role in intracellular signaling and gene expression or in
 linking chromatin to the nuclear membrane. May function in the
 cytoplasmic partitioning of proteins (By similarity).
 CC complex composed of a presenilin homodimer (PSEN1 or PSEN2),
 nicastrin (NCSTN), APH1 (APH1A or APH1B) and PEN2. Such minimal
 complex is sufficient for secretase activity, although other
 components may exist. Interacts with DCK3. Interacts with
 HERPUD1, F11A and F11B (By similarity).
 CC SUBCELLULAR LOCATION: Integral membrane protein. Golgi and

Db	57 QNNIQQVDDQDEEDEELTLKYGAKEVIMLFVPTLCMVVVATIKSVSFYRKDGQIY 116	Db	1 : : : : : : : : : : : 60
Qy	116 TPFTDDETTGQRALHSILNAIMSVTIVMTILWVLYKRYCYKVTIHLWLISSLWF 175	Qy	142 VIWMMTLLWVLYKRYCYKVTIHLWLISSLWFPSFVYLGEBVFTYNAVDITVALL 201
Db	117 TPFTDDETTGQRALHSILNAIMSVTIVMTILWVLYKRYCYKVTIHLWLISSLWF 176	Db	61 VIWMMTLLWVLYKRYCYKVTIHLWLISSLWFPSFVYLGEBVFTYNAVDITVALL 120
Qy	176 PFSFIVLGEBVFTYNAVDITVALLWVLYKRYCYKVTIHLWLISSLWF 235	Qy	202 IWNFGVYGMISPHWKQPLRQOAYLIMISALM 261
Db	177 PFSFIVLGEBVFTYNAVDITVALLWVLYKRYCYKVTIHLWLISSLWF 236	Db	121 IWNFGVYGMICHLWKGPLRQOAYLIMISALM 180
Qy	236 VPIKYLPEWTLAVLAVISVYDVLAVLCLGKPLRQOAYLIMISALM 295	Qy	262 LCIKGPMVMTAQERNETIPALYSSTMWLNMAGDPEAQRRVSKNSKHAESTE 321
Db	237 VPIKYLPEWTLAVLAVISVYDVLAVLCLGKPLRQOAYLIMISALM 296	Db	181 LCPKGPRJLVLVTAQERNETIPALYSSTMWL 233
Qy	296 VMAEGDPEAQRRVSKNSKHAESTERESQDTVAENDGGPSEEMEAQDSH-GPHRSTP 355	Qy	322 RQSDTYA---ENDGGPSEEMEAQDSH-GPHRSTP 376
Db	297 VMAEGDPEAQRRVSKNSKHAESTERESQDTVAENDGGPSEEMEAQDSH-GPHRSTP 356	Db	234 QENQDQVAPTAGPDDGGTPRAWNQOQHQLGPMSQEDSRERIQIQLPSARPPVEDDE 293
Qy	356 ESSRAAVOALPSNSQTSDPEPGRVKLGIGDIFYSLVNGKASATASGDWNTTACFVAIL 415	Qy	377 RGKVLGQDFIYSLVNGKASATASGDWNTTACFVAIL 436
Db	357 ESSRAAVOALPSNSQTSDPEPGRVKLGIGDIFYSLVNGKASATASGDWNTTACFVAIL 416	Db	294 RGYKLGQDFIYSLVNGKASATASGDWNTTACFVAIL 535
Qy	416 IGLCLTLLAIFKKALPALPSITGIVFATYLVQFMDQLAHQFYI 467	Qy	437 ISITFGLVYFYFADYLVQFMDQLAHQFYI 467
Db	417 IGLCLTLLAIFKKALPALPSITGIVFATYLVQFMDQLAHQFYI 468	Db	354 ISITFGLVYFYFADYLVQFMDQLAHQFYI 384
RESULT 2			
073869	PRELIMINARY; PRT; 384 AA.	073869	OBNS58
AC	073869; 07 (Tremblrel. 07, Created)	AC	OBNS58;
DT	01-AUG-1998 (Tremblrel. 07, Last sequence update)	DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)	DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE	PSI protein (fragment).	DE	DBP
GN		GN	PS
OS	Cyprinus carpio (Common carp); Craniata; Vertebrates; Euteleostomi;	OS	Branchiostoma floridae (Florida lancelet) (Amphioxus)
OC	Bukaryota; Metazoa; Chordata; Ostariorphysi; Cypriniformes;	OC	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC	Cyprinidae; Cyprinus.	OC	Branchiostome.
OX	NCBI_TaxID=962;	OX	NCBI_TaxID=7739;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A. PubMed=9674592;	RP	SEQUENCE FROM N.A. PubMed=11733140;
RX	MEDLINE=98337349; Pubmed=9674592;	RX	MEDLINE=21590369; Pubmed=11733140;
RA	Archer S., Hirano J., Diss J.K.J., Fraser S.P., Djangoz M.B.A.;	RA	Albalat R., Martinez-Mir A., Canestro C., Gonzalez-Duarte R.,
RT	"Expression and localization in the fish retina of a homologue of the	RT	"Characterization of the amphioxus presenilin gene in a high gene-density genomic region illustrates duplication during the vertebrate lineage."
RT	Alzheimer's related P51 gene.;"	RT	RT
RL	NeuroReport 9:2045-2051 (1998).	RL	Gene 279:157-164 (2001).
DR	EMAIL; Y17128; CAAT6641.1; -.	DR	EMBL; AF269891; AXL40416.1; -.
DR	MEROPS; A22_001; C membrane; IEA.	DR	EMBL; AF269890; AXL40416.1; JOINED.
DR	GO; GO:0016020; C membrane; IEA.	DR	GO; GO:0016020; C membrane; IEA.
DR	GO; GO:007242; P: intracellular.	DR	GO; GO:003700; P: transcrip-
DR	InterPro; IPR006699; Peptidase_A22.	DR	DR
DR	InterPro; IPR001608; Peptidase_A22A.	DR	GO; GO:0007242; P: intracellular signaling cascade; IEA.
DR	InterPro; IPR001608; Peptidase_A22A.	DR	GO; GO:0003555; P: regulation of transcription, DNA-dependent; IEA.
DR	PRINTS; PRO1080; Presenilin; 1.	DR	InterPro; IPR00847; HTH LVR.
DR	PRINTS; PRO1072; PRESENTIN.	DR	InterPro; IPR0063; Peptidase_A22.
DR	SMART; SM00730; PSN; 1.	DR	InterPro; IPR00108; Peptidase_A22.
FT	NON-TER 1	FT	DR
FT	VARIANT 5 5 I -> V.	FT	PRINTS; PRO1072; PRESENTIN.
FT	VARIANT 5 5 A -> S.	FT	DR
FT	VARIANT 56 56 A -> V.	FT	SMART; SM00730; PSN; 1.
FT	VARIANT 60 60 S -> G.	FT	DR
FT	VARIANT 63 63 V -> L.	FT	SEQUENCE; PS00044; HTH LVR FAMILY; 1.
FT	VARIANT 83 83 G -> A.	FT	SEQUENCE; PS00044; MW; 903794b0302859b4 CRC64;
FT	VARIANT 118 118 A -> S.	FT	Query Match 57.2%; Score 1368; DB 5; Length 504;
FT	VARIANT 200 200 P -> T.	FT	Best Local Similarity 58.8%; Pred. No. 2.2e-105; Mismatches 56; Indels 36; Gaps 7;
SQ	SEQUENCE 384 AA; 43276 MW; F97EEFB24B31FDAA CRC64;	SQ	Matches 275; Conservative 56; Mismatches 101; Indels 36; Gaps 7;
Qy	64.0%; Score 1539.5; DB 13; Length 384;	Qy	27 RSONDREROPHNDRSLRGPPLSNGRPGNSROVEQDDEBBLTYGAKHIVMLP 86
Qy	Best Local Similarity 79.5%; Pred. No. 5.6e-119; Mismatches 40; Indels 13; Gaps 6;	Db	46 RSQQQIENTPDGDREBAG---DGGEDHGRIR---EBEDEDETMKYGAKEVIMLP 98
Matches 311; Conservative 27; Mismatches 40; Indels 13; Gaps 6;	Qy	87 VPVTLQWVWVATIKSVSFYRKDG-QLIITPFDIDETVGQRALHSILNAIMSVIVM 146	

Db 99 APVSLCMWAVVATISSTFYEKGVLYTFHEEGASTAKVGDSLNGALIMGVILM 158
 QY 147 TLLVVKYRKVKVHAWLTISSLLUFFSFSIYGEVFKNVYNAVDYTVALIWNFG 206
 Db 159 TPLVLVVKYRKVKFIRGWLISLSSMLFLFAYIVYGENLQYNPDCYITLAVIWNFG 218
 QY 207 VVGMISIHWKGFLRQOAYLIMISALMVLVYKYLEWTAVALAVLAVISVTDLAVICLK 266
 Db 219 AVGMVCHWKGLLQOAYLIVISALMVLVYKFLPDWTWFLGALISLYDVLAVLCPKG 278
 QY 267 PIRMLVETQAQNETLPALYSSTMWLVNAEGDPEAQRSNSKHESTERES-- 324
 Db 279 PLKLVETQAQNEPITPALISSTMMWVKAQDSPEAKKKKKRRAQDGPDQAGA 338
 QY 325 -QDTVAENDDGFSEEEQAQR--DSHGPHR----- STPESRAAVQELSSILA-- 370
 Db 339 PAGAVGGEDEGGPDWNEKSFQOPTRPNRGGNSDASVNSEDARQAQNLNSNGLSPS 398
 QY 371 -----GDPERGVKULGLGPIFIYFLVGSATSGDMNTTACFVALLIGC 419
 Db 399 GNOQQQOMEREBEDBEBERGVKULGLGPIFIYFLVGRAS- SNGDNTTACFVALLIGC 456
 QY 420 LLLIAIPKALPALPISIYFLVYFATMYLVOFMDQIAHFIYI 467
 Db 457 LLLIAIPKALPALPISIYFLVQFATANLVFTDALSQQTV 504
 RESULT 4
 Q90X07
 PRELIMINARY; PRT; 451 AA.
 AC Q90X07;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE presenilin_2;
 OS Gallus gallus (Chicken).
 OC Bukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC NCBI_TAXID=9031;
 RN 1
 RP SEQUENCE FROM N.A.
 RA Korade Mitrani Z., Keryanov S., Lovelock J., Corey S.J.;
 RT "Cloning of chicken presenilins.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY03493; AAKG5409_1; -
 GO: GO:000620; C:membrane; IEA.
 DR GO:0007242; P: intracellular signaling cascade; IEA.
 DR InterPro; IPR006639; Peptidase_A22.
 DR InterPro; IPR001108; Peptidase_A22A.
 DR Pfam; PF01080; presenilin_1.
 DR PRINTS; PRO1072; PRESNILIN.
 DR SMART; SM00730; PSN_1.
 DR SWIFT; SW00730; PSN_1.
 SQ SEQUENCE 451 AA; 50496 MW; 534E634C62788B0 CRC64;
 Query Match 56.9%; Score 1361.5; DB 13; Length 451;
 Best Local Similarity 59.7%; Pred. No. 6.6e-105;
 Matches 283; Conservative 43; Mismatches 71; Indels 77; Gaps 7;
 QY 3 ELPAPLSPYFORQMSDHNLSNTVRSQNDNERQERBENDRSFLGHPEPLSNGRPGNSR-- 60
 Db 25 DSSPPVSYQDQIQAEST-----TREQQTIRKROT-----GSSRSP 58
 QY 61 -QVVEDD-----PDEDEBLTQKGAKEVIMLFWPVTLCMVWVATKSVF 66
 Db 59 INVADASDSDVRSALNEEBELTQKGAKEVIMLFWPVTLCMVWVATKSVF 118
 QY 107 TRKDGLIYTFPTEDETVGRALHSLNAAIMSVIWTMFLVYKRCYVTHAWL 166
 Db 119 TFKGOLIYTFPTEDETVGRALHSLNAAIMSVIWTMFLVYKRCYFIRGML 178
 QY 167 TLLVVKYRKVKVHAWLTISSLLUFFSFSIYGEVFKNVYNAVDYTVALIWNFG 206
 QY 147 TLLVVKYRKVKVHAWLTISSLLUFFSFSIYGEVFKNVYNAVDYTVALIWNFG 206
 Db 159 TPLVLVVKYRKVKFIRGWLISLSSMLFLFAYIVYGENLQYNPDCYITLAVIWNFG 218
 QY 239 IMISALMVLVFKYLPEWASVWLGAISSYDIALVFLGKPLRMXETAQERNQPIFFAL 298
 QY 287 IVSTMVULVNMRGDPPEQRRYKNSCHNAISTERISQDTVAENDGGFSSEWEAQRS 346
 Db 299 IVSSAMINIVGMAPDTIAK-----GOSQGAWDABER 331
 QY 347 HLGPHRSTPESRAVQESESS-----ILAGDPERGVKULGDFPFIYFLVGSATA 400
 Db 332 E-NHSSTHSQSDQILDRTRSPASHPITLBBEEBERGVKULGDFPFIYFLVGSATA 389
 QY 401 SGDNTTACFVALLIGCILTULLAFLKKALPALPISITFGLVFLVPAIDVWQ 454
 Db 390 SGDNTTACFVALLIGCILTULLAFLKKALPALPISITFGLVFLVPAIDVWQ 443
 RESULT 5
 Q8M559 PRELIMINARY; PRT; 525 AA.
 ID Q8M559
 AC Q8M559;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Presenilin.
 GN PS
 OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
 OC Eukaryota; Metzoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 OX NCBI_TAXID=7739;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2150369; PubMed=1173340;
 RA Martinez-Mir A., Canistro C., Gonzalez-Duarte R., Albalat R.;
 RT "Characterization of the amphioxus presenilin gene in a high gene-density genomic region illustrates duplication during the vertebrate lineage.";
 RT Gene 279:157-164 (2001).
 RL EMBL: AP36991; AAU40414;
 DR EMBL; AP36990; AAU40414; JOINED.
 DR GO; GO:001020; C:membrane; IEA.
 DR GO; GO:000700; P:transcription factor activity; IEA.
 DR GO; GO:0007242; P: intracellular signaling cascade; IEA.
 DR InterPro; IPR00847; HTH_LYSR.
 DR InterPro; IPR006639; Peptidase_A22.
 DR InterPro; IPR00108; Peptidase_A22A.
 DR PRINTS; PRO1072; PRESNILIN.
 DR SMART; SM00730; PSN_1.
 DR PROSITE; PS0044; HTH_LYSR_FAMILY; 1.
 SQ SEQUENCE 525 AA; 57598 MW; 2B14CF77A80F07DE CRC64;
 Query Match 56.9%; Score 1360.5; DB 5; Length 525;
 Best Local Similarity 56.6%; Pred. No. 9.6e-105;
 Matches 277; Conservative 56; Mismatches 99; Indels 57; Gaps 8;
 QY 27 RSDQDNRBRQEEHNDRRGIGHPBPLSNGRPGNSRQYVEQDEDEBLTQKGAKEVIMLF 86
 Db 46 RSGQIQENTPDGADRREG---DGGBDKGIRH--DDEBEDETMFLKGAKEVIMLF 98
 QY 87 VPTPLCMWVWVATKSVFVYTRKDGLIYTFPTEDETVGRALHSLNAAIMSVIWTM 146
 Db 99 APVSLCMWAVVATISSTFYEKGVLYTFHEEGASTAKVGDSLNGALIMGVILM 158
 QY 147 TLLVVKYRKVKVHAWLTISSLLUFFSFSIYGEVFKNVYNAVDYTVALIWNFG 206
 Db 159 TPLVLVVKYRKVKFIRGWLISLSSMLFLFAYIVYGENLQYNPDCYITLAVIWNFG 218
 QY 207 VVGMISIHWKGFLRQOAYLIMISALMVLVYKYLEWTAVALAVLAVISVTDLAVICLK 266

Db	219	AVENVCVHWKGPLILQQLQYLIVISALMALVFKKLPDFTTWFLGAIISYDVLAVLCPKG	278	QY	235	UPIKIKUPETWILAVISYDVLVATLCKPLRMLVETAQERNELFPALIYSMM	294
Db	267	PIRMLVETQAERETLFALIYSSTMWVLLVMNAGDPAQQRYSKNSKNAES-----	319	QY	272	UPIKIKUPETWILAVISYDVLVATLCKPLRMLVETAQERNELFPALIYSMM	294
Db	279	PLKVLVETQAERNPFPALIYSSTMWVLLVMNAGDPAQQRYSKNSKNAES-----	319	QY	279	PLKVLVETQAERNPFPALIYSSTMWVLLVMNAGDPAQQRYSKNSKNAES-----	319
Db	320	--TRESEQDT-----	352	QY	295	LMMAEGDPBEAQRVS-----	347
Db	339	FRLIDNEAGSTGDDADAFDSARAGAAGCSEEERGCPDWNESRGFOPTRRPNNGNASDAS	398	QY	332	PTMADGDPDKKKKKKKKKKKGQDQNSVTTPLGKOT-----	389
Db	353	--STPESRRAVQELSSSIA-----	398	QY	348	LSPHRSTPESRRAVQEL-----	373
Db	399	:::VNSEDARQAQNLSNGRISPGSGNQQQQMEEDEDERGKVGLGPIFYSVLSGRAS-	457	QY	390	LIAQSQDSARNAVAQAFGMDVKPRTRNAVSHTTWNTTNSARVIAATKQAGVESAVR	449
Db	399	TASQDWNTTIACTCVALIGLICLTLIAIFKALPALPISITFGLVYPATDYLQPRMD	458	QY	374	--	392
Db	458	-SNQDWNTTACVALIGLICLTLIAIFKALPALPISITFGLVNFATANLVTPTD	516	QY	450	VNVDQRDGAVVANSRSQNSRTRPALRPLSDSIQDDSEBERGVGLGQDFIFGV	509
Qy	459	QLAFHQFYI 467	516	QY	393	VGKASATASGDNNTTACVALIGLICLTLIAIFKALPALPISITFGLVYPATDYL	452
Db	517	ALASQQTV 525	516	QY	510	VGRKAS- SNGDWNTTACVALIGLICLTLIAIFKALPALPISITFGLVNFATSSL	567
QY	517	ALASQQTV 525	516	QY	453	WQPFDQLAHQFYI 467	567
Db	568	VQPFMDLILASEQVYI 582	567	Db	568	VQPFMDLILASEQVYI 582	567
RESULT 6							
QGCU38		PRELIMINARY;	PRT;	582 AA.	Q8HZ65		Q8HZ65
ID	09G38				ID	Q8HZ66	
AC	09G38;				AC	Q8HZ66;	
DT	01-MAR-2001 (TREMBrel. 16, Created)				DT	01-MAR-2003 (TREMBrel. 23, Last sequence update)	
DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)				DT	01-MAR-2003 (TREMBrel. 23, Last sequence update)	
DE	Presentinin.				DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)	
GN	PS.				DE	Presentinin (Fragment).	
OS	Helix lucorum.				OS	Oryctolagus cuniculus (Rabbit)	
OC	Bukaryota; Metazoa; Gastropoda; Pulmonata; Stylo-matophora;				OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Sigmatethra; Helicoidea; Helicidae; Helix.				OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	
NCBI_Taxid	31229;				NCBI_Taxid	9986;	
RN	[1]				RN	[1]	
RP	SEQUENCE FROM N.A.				RP	SEQUENCE FROM N.A.	
RA	Rogaeva E. I., Riazanskaya N. N., Dvoranchikov G., Grigorenko A. P.,				RA	Al-Khedhairi A.A., Arfin M., Al-Dukhyil A.B.;	
RA	Tyrsin O.; "Presentinin gene isolated from mollusk <i>Helix lucorum</i> .";				RA	Molecular cloning and sequencing of the rabbit presenilin-1 cDNA	
RA	Submitted (Oct-1999) to the EMBL/GenBank/DDBJ databases.				RT	RT fragment." (JUL-2002) to the EMBL/GenBank/DDBJ databases.	
RL	EMBL; APR19781; AUG2518.1; -				RL	Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.	
DR	GO; GO:0016202; C:membrane; IEA.				DR	EMBL; AY134851; AAN0498.1; -	
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.				DR	GO; GO:0001620; C:membrane; IEA.	
DR	InterPro; IPR006539; Peptidase_A22.				DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.	
DR	InterPro; IPR0108; Peptidase_A22A.				DR	InterPro; IPR006539; Peptidase_A22.	
DR	InterPro; IPR0108; Peptidase_A22A.				DR	InterPro; IPR0108; Peptidase_A22A.	
DR	InterPro; IPR0108; Peptidase_A22A.				DR	InterPro; IPR0108; Peptidase_A22A.	
DR	PF01080; Presentinin; 1.				DR	PF01080; Presentinin; 1.	
DR	PRINTS; PRO1072; PRESENTIN.				DR	SMART; SM00730; PSN; 1.	
DR	SMART; SM00730; PSN; 1.				FT	NON-TER	
DR	SMART; SM00730; PSN; 1.				FT	NON-TER	
DR	SEQUENCE 582 AA; 63782 MW; 079343E7452199F0 CRC64;				FT	NON-TER	
QY	Query Match 51.9%; Score 1240.5; DB 5; Length 582; Best Local Similarity 48.1%; Pred. No. 1.1e-94; Matches 267; Conservative 73; Mismatches 108; Indels 107; Gaps 11;				FT	NON-TER	
Db	9	SYRQNAQNSEDNLNLTW-----RSQDNRERQEHNDRSLRQHPPPLS-----NGR	54	QY	112	QIYTPFETEDTETVGORALHSTINAATMSIVVMTILLVWVYKRYKVTHAWLISL	171
Db	39	SRVQLQNSTEDDY-NAPEATVVDPRSQGDASSRNSHQSHTQCSRSPRANPTE	97	QY	1	QIYTPFETEDTETVGORALHSTINAATMSIVVMTILLVWVYKRYKVTHAWLISL	60
QY	55	POGNSRQVEQDEDEELTLKYGAKHIMLFWPTVLCMVVATIKVSFVTRKGQLI	114	QY	172	LILFFPSIYLGKRVFKTYNAVDYITVALLWNGVGMISIHWKGDLRQOAYLMTSA	231
Db	98	PSGGN---QDDDEE-TLYGAKHIMLFWPTLWVWVATISITVYTSVSGWLI	151	QY	61	LILFFPSIYLGKRVFKTYNAVDYITVALLWNGVGMISIHWKGDLRQOAYLMTSA	220
QY	115	YTPFTEDTETVGORALHSTINAATMSIVVMTILLVWVYKRYKVTHAWLISL	174	QY	232	LALVFLPKLPEN 244	
Db	152	YTPFTEDTETVGORALHSTINAATMSIVVMTILLVWVYKRYKVTHAWLISL	174	QY	121	LALVFLPKLPEN 133	
QY	175	PEFSPIYGEVEKVNQVNAVDYITVALLWNGVGMISIHWKGDLRQOAYLMTSA	234	QY	212	FFPSMFLQILRRAVNPDMVYVTAIWMNGFGLFCITHWKQPLQIQLQAYLIVSVALVA	271

motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral hemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding the wild type sequences, or vectors that express them or containing antisense sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g. for affinity purification and in immunoassays. (Updated on 25-MAR-2003 to correct PI field.)

CC CC motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral hemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding the wild type sequences, or vectors that express them or containing antisense sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g. for affinity purification and in immunoassays. (Updated on 25-MAR-2003 to correct PI field.)

CC CC

XX XX

SQ Sequence 467 AA;

PS

Query Match 99.7%; Score 2365; DB 2; Length 467;

Best Local Similarity 99.8%; Pred. No. 2.7e-234; Mismatches 0; Indels 0; Gaps 0;

Matches 466; Conservative 1; MisMatches 0;

QY 1 MTELAPALSYFONAQMSEDNHLSNVRSONDRQERQENDRRSLIGHPPPLNSRPOQNSR 60

Db 1 MTELAPALSYFONAQMSEDNHLSNVRSONDRQERQENDRRSLIGHPPPLNSRPOQNSR 60

QY 61 QVVEDDEBEDBELTUKYAKHVINLFPVPLCMWVWATIKSVSFYTRKDGQLIYPTPE 120

Db 61 QVVEDDEBEDBELTUKYAKHVINLFPVPLCMWVWATIKSVSFYTRKDGQLIYPTPE 120

QY 121 DTETYGORALHSILNAIMISVITYVNTILLVLUKYRKYVHAWLILSSLLLFFPSI 180

Db 121 DTETYGORALHSILNAIMISVITYVNTILLVLUKYRKYVHAWLILSSLLLFFPSI 180

QY 181 YLGEVFKTNAVADYITVALLIINFGVWVNMISIHWKGPLRQOAYLMISALMVFYK 240

Db 181 YLGEVFKTNAVADYITVALLIINFGVWVNMISIHWKGPLRQOAYLMISALMVFYK 240

QY 241 LPENWALILAVIYSTYDYLAVLCKGPKLMLVTAQERNETLPALIYSTMWLNAAE 300

Db 241 LPENWALILAVIYSTYDYLAVLCKGPKLMLVTAQERNETLPALIYSTMWLNAAE 300

QY 301 GDEPQRQRYSKNSKNEAESTERESQDTAENDDGGESEWEAORDSHGPHRSTPESRAA 360

Db 301 GDEPQRQRYSKNSKNEAESTERESQDTAENDDGGESEWEAORDSHGPHRSTPESRAA 360

QY 361 VOELSSSIAGEDDEBERGKGLGDFIYVLUVGKASATASGWNNTTACFVAILIGCL 420

Db 361 VOELSSSIAGEDDEBERGKGLGDFIYVLUVGKASATASGWNNTTACFVAILIGCL 420

QY 421 TLLIAIFKKALPALPISITFGLVYFATDYLVOPFMQDQLAHQFYI 467

Db 421 TLLIAIFKKALPALPISITFGLVYFATDYLVOPFMQDQLAHQFYI 467

RESULT 2

AAW27176 ID AAW27176 standard; protein; 467 AA.

AC XX

AAW27176; DT 09-DEC-1997 (first entry)

XX Human S182 gene, PstI locus, product related to Alzheimer's disease.

XX Mutant; antisense; antibody; vaccine; Alzheimer's disease.

OS Homo sapiens

XX W09708319-A1.

XX 06-MAR-1997.

XX 03-SEP-1996; PP 96W0-US014114.

PR 31-AUG-1995; 95US-0003054P.

PR 30-AUG-1995; 96US-00706344.

XX (GEHO) GEN HOSPITAL CORP.

XX PI Tanzi RE, Wasco W;

XX DR WPI; 1997-179276/16.

XX N-PSDB; AAT85332.

XX PT Chromosome 14, early-onset familial Alzheimer's disease gene PS1 mutants - useful for diagnosing likelihood of developing Alzheimer's disease, also anti-sense sequences, antibodies and vaccines to delay onset.

XX

PS Claim 12; Page 72-73; 99pp; English.

XX

CC The present sequence represents the human S182 gene, PS1 locus, product.

CC Mutant PS1 produces a gene product that increases the probability of Alzheimer's disease. A nucleic acid sequence able to hybridise to

CC sequences coding for a mutant PS1 polypeptide can be used as probes for

CC diagnosing an increased likelihood of contracting Alzheimer's disease.

CC Antibodies against the mutant polypeptide can also be used for this

CC purpose. Vectors containing or expressing a nucleic acid molecule, a

CC protein or antibody specific for mutant PS1 can be administered to a

CC patient to reduce the likelihood, or delay the onset, of Alzheimer's

CC disease, e.g. anti-sense RNA expression can be used to decrease

CC expression of the PS1 peptide. Transgenic animals expressing the

CC Alzheimer's disease protein can be used to test candidate therapeutics

CC and to investigate the normal role of PS1. The PS1 peptide may also be

CC included in pharmaceutical compositions (vaccines) for Alzheimer's

CC disease therapy.

XX

SQ Sequence 467 AA;

PS

Query Match 99.7%; Score 2364; DB 2; Length 467;

Best Local Similarity 99.8%; Pred. No. 3.4e-234; Mismatches 1; Indels 0; Gaps 0;

Matches 466; Conservative 0; MisMatches 1;

QY 1 MTELAPALSYFONAQMSEDNHLSNVRSONDRQERQENDRRSLIGHPPPLNSRPOQNSR 60

Db 1 MTELAPALSYFONAQMSEDNHLSNVRSONDRQERQENDRRSLIGHPPPLNSRPOQNSR 60

QY 61 QVVEDDEBEDBELTUKYAKHVINLFPVPLCMWVWATIKSVSFYTRKDGQLIYPTPE 120

Db 61 QVVEDDEBEDBELTUKYAKHVINLFPVPLCMWVWATIKSVSFYTRKDGQLIYPTPE 120

QY 121 DTETYGORALHSILNAIMISVITYVNTILLVLUKYRKYVHAWLILSSLLLFFPSI 180

Db 121 DTETYGORALHSILNAIMISVITYVNTILLVLUKYRKYVHAWLILSSLLLFFPSI 180

QY 181 YLGEVFKTNAVADYITVALLIINFGVWVNMISIHWKGPLRQOAYLMISALMVFYK 240

Db 181 YLGEVFKTNAVADYITVALLIINFGVWVNMISIHWKGPLRQOAYLMISALMVFYK 240

QY 241 LPENWALILAVIYSTYDYLAVLCKGPKLMLVTAQERNETLPALIYSTMWLNAAE 300

Db 241 LPENWALILAVIYSTYDYLAVLCKGPKLMLVTAQERNETLPALIYSTMWLNAAE 300

QY 301 GDEPQRQRYSKNSKNEAESTERESQDTAENDDGGESEWEAORDSHGPHRSTPESRAA 360

Db 301 GDEPQRQRYSKNSKNEAESTERESQDTAENDDGGESEWEAORDSHGPHRSTPESRAA 360

QY 361 VOELSSSIAGEDDEBERGKGLGDFIYVLUVGKASATASGWNNTTACFVAILIGCL 420

Db 361 VOELSSSIAGEDDEBERGKGLGDFIYVLUVGKASATASGWNNTTACFVAILIGCL 420

QY 421 TLLIAIFKKALPALPISITFGLVYFATDYLVOPFMQDQLAHQFYI 467

Db 421 TLLIAIFKKALPALPISITFGLVYFATDYLVOPFMQDQLAHQFYI 467

RESULT 3

AAW05733 ID AAW05733 standard; protein; 467 AA.

XX
AC AAW05733;
XX
DT 25-MAR-2003 (revised)
DT 23-JUN-1997 (first entry)
XX
DE Presenilin-1-1.
XX
KW Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD; depression; antibody; gene expression modulator; therapy.
OS Homo sapiens.
XX
PN WO9634099-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96WO-CA000263.
XX
PR 28-APR-1995; 95US-00431048.
PR 28-JUN-1995; 95US-00459359.
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX
PI St Georgeyvslap PH, Fraser PB, Rommens JM;
XX
DR WPI: 1996-497631/49.
XX
PT New presenilin genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS Claim 2; Page 128-130; 178pp; English.
XX
CC AAW05733 and AAW05734 represent the two different forms of wild type human presenilin-1 (PS-1). The form represented by AAW05734 results from alternate splicing of the genomic DNA sequence. AAW05762 represents the coding sequence for wild type human PS-2. The presenilins are a family of highly conserved integral membrane proteins with a common structural motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding these sequences can be used for diagnosis of these diseases. These proteins, or vectors that express them or containing antisense sequences, antibodies selective for mutant forms of these proteins (such as AAW05736) and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g. for affinity purification and in immunassays. (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 467 AA;

Query Match 99.5%; Score 2378; DB 2; Length 467;
Best Local Similarity 99.6%; Preq. 1, 48-233; 1; Mismatches 0; Indels 0; Gaps 0;

Matches 455; Conservative 1; PS
1 MTELAPLAPSQYQNAOMSDENDHLSNTVRSQNDRERQEHNDRLSIGHPPPLSPQRQNSR 60
1 MTELAPLAPSQYQNAOMSDENDHLSNTVRSQNDRERQEHNDRLSIGHPPPLSPQRQNSR 60
QY 61 QWVEDEBDELTLKIGAKHVKMLFVPTLICMVWVATIKSISFYRKDGQIYTFTE 120
61 QWVEDEBDELTLKIGAKHVKMLFVPTLICMVWVATIKSISFYRKDGQIYTFTE 120
Db 121 DTEVGQRALHSINAAIMTIVVWMTLIVVVKYRCYKVIAHAWLISLILLFFPSI 180
Db 121 DTEVGQRALHSINAAIMTIVVWMTLIVVVKYRCYKVIAHAWLISLILLFFPSI 180
QY 181 YLGEVFKTYNAVDYITVALLINFGVYGMISIHMKGLRLQAYLIMISALMVFY 240

XX
PS RESULT 4
XX
ID AAW41430 standard; protein; 467 AA.
XX
AC AAW41430;
XX
DT 04-JUN-1998 (first entry)
XX
DE PS1/467 protein.
XX
KW Presenilin peptide; PS1/429; immunogen; immune response; PS1 gene; apoptosis; PS1/467.
XX
OS Homo sapiens.
XX
PN WO9746678-A1.
XX
PD 11-DEC-1997.
XX
PR 03-JUN-1997; 97WO-US009272.
XX
PR 06-JUN-1996; 96US-0065296.
PR 18-JUL-1996; 96US-00683315.
XX
PA (FARB) BAYER CORP.
XX
PI Davis JN, Chisholm JC, Drache B;
XX
DR WPI: 1998-04286/04.
DR N-PSDB; AAV17358.
XX
PT DNA encoding presenilin peptide PS1/429 and its analogues - useful for diagnosis and treatment of Alzheimer's disease.
XX
PS Claim 7; Fig 2; 77pp; English.
XX
CC This sequence is the PS1/467 presenilin peptide. This sequence is specifically stated as not being in the nucleic acid of the invention, which encodes the PS1/429 presenilin peptide PS1/429 (II). Cells transformed with the DNA are used to produce recombinant (II) and analogues useful e.g. as immunogens for generating an immune response against PS1/429. (II) is a new product of the PS1 gene, mutations in which cause Alzheimer's disease (AD). The nucleic acids are generally useful as probes particularly for detection and quantification of PS1/429, hybridise with probes isolated for sequencing. Antibodies (Ab) can also be diagnosed at the protein level using Ab as immunassay reagents. Ab can also be used to identify epitopes and for affinity purification of peptides. Antisense nucleic acid may also be used to regulate expression of the PS1/429 gene, and both nucleic acids and peptides are useful as size markers in electrophoresis, chromatography etc. The transgenic animals are used as models for AD, e.g. for testing drugs. Regulators of

the P51/429 gene or polypeptide can be used to treat e.g. AD or diseases involving mitochondrial pathology, apoptosis and neurodegeneration. Typical regulators are antisense sequences, ribozymes, aptamers, synthetic or natural compounds. (II) may also be used to target other coding sequences to particular cellular locations

XX Sequence 467 AA;

Query Match 99.5%; Score 2378; DB 2; Length 467;
Best Local Similarity 99.6%; Pred. No. 1.4e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC MTELPAPLSYFQANQMSDHNLSNTVRSONDNRQHNDRQHNSLGHPEPLNSRPOQNSR
CC 1 MTELPAPLSYFQANQMSDHNLSNTVRSONDNRQHNDRQHNSLGHPEPLNSRPOQNSR 60
CC QY 61 QVTFQDEEDEELFLKYGAKHVMILFVPTLCKMVWATKSYFVYRDKQQLYKPFTE 120
Db 61 QVVFQDEEDEELFLKYGAKHVMILFVPTLCKMVWATKSYFVYRDKQQLYKPFTE 120
Db 121 DTEVYQGRALHSINAAMISVIVVMTILWVLYKRYCYYHAWLTLSSLLFFPSI 180
QY 181 YLGEVFKTNNVAUDYITVAILINLNGVYGMISHWKGQLRQOAYLIMISALMAYFIK 240
Db 181 YLGEVFKTNNVAUDYITVAILINLNGVYGMISHWKGQLRQOAYLIMISALMAYFIK 240
QY 241 LPENTAWLIAVSVYDYLAVLCLKGPARMVLTQBNETRPAlysSTMWLYMAB 300
Db 241 LPENWAWLIAVSVYDYLAVLCLKGPARMVLTQBNETRPAlysSTMWLYMAB 300
QY 301 GDPEAQQRYSKNSKNAESTERESQPTAENDGGFSEWABORDSINGRSPSTPSRAA 360
Db 301 GDPEAQQRYSKNSKNAESTERESQPTAENDGGFSEWABORDSINGRSPSTPSRAA 360
QY 421 TLLIAIFKPKALPALPISITFLGLVYFATDLYVQPFMDQLAHQFYI 467
Db 421 TLLIAIFKPKALPALPISITFLGLVYFATDLYVQPFMDQLAHQFYI 467

RESULT 5
ID AAW23964
ID AAW23964 standard; protein; 467 AA.
XX AAW23964;
XX DT 20-JUL-1998 (first entry)
XX DE Human presenilin-1.
XX KW Presenilin-1; P51 gene; human; familial Alzheimer's disease; FAD; cerebral haemorrhage; schizophrenia; depression; epilepsy; mental retardation; diagnosis; therapy; transgenic animal.
XX OS Homo sapiens.
XX FH Key-difference Location/Qualifiers
FT Misc-difference 26-.29
/note= "residue 26-29 deletion, resulting from alternative splicing"
FT Misc-difference 79
/note= "Ala79Xaa mutation site"
FT Domain 82-.100
/label= "TM1"
FT Misc-difference 82
/note= "transmembrane domain 1"
FT Misc-difference 95
/note= "Val82Ileu mutation site"

FT Domain 101-.132
/note= "TM1-2"
FT /note= "hydrophilic loop"
FT Misc-difference 115
/note= "Tyr115His mutation site"
FT Domain 133-.154
/note= "transmembrane domain 2"
FT Misc-difference 139
/note= "Met139Val mutation site"
FT Misc-difference 143
/note= "Ile143Thr mutation site (Claim 18)"
FT Misc-difference 145
/note= "Met46Val mutation site"
FT Misc-difference 146
/note= "Met146Leu mutation site (Claim 18)"
FT Domain 155-.163
/note= "His163Arg mutation site"
FT Misc-difference 163
/note= "Hydrophilic loop"
FT Misc-difference 164-.183
/note= "TM3"
FT Misc-difference 171
/note= "His163Tyr mutation site"
FT Misc-difference 177
/note= "Leu171Pro mutation site (Claim 18)"
FT Domain 184-.194
/note= "transmembrane domain 3"
FT Misc-difference 195-.212
/note= "Phel17Ser mutation site (Claim 1)"
FT Domain 209
/note= "Gly209Val mutation site"
FT Misc-difference 211
/note= "TM3-4"
FT Domain 213-.220
/note= "hydrophilic loop"
FT Domain 221-.238
/note= "TM4-5"
FT Domain 231
/note= "TM5"
FT Misc-difference 231
/note= "transmembrane domain 5"
FT Domain 239-.243
/note= "Ala231Thr mutation site"
FT Domain 244-.262
/note= "hydrophilic loop"
FT Misc-difference 246
/note= "transmembrane domain 6"
FT Misc-difference 246
/note= "Ala246Glu mutation site"
FT Misc-difference 257
/note= "Asp257Ala mutation site, associated with residue 258-290 deletion (Claim 1)"
FT Misc-difference 258-.290
/note= "residue 258-290 deletion mutant, associated with Asp257Ala mutation (Claim 1)"
FT Misc-difference 260
/note= "Ala60Val mutation site (Claim 18)"
FT Domain 263-.407
/note= "TM6-7"
FT Misc-difference 263
/note= "hydrophilic loop"
FT Misc-difference 264
/note= "Cys263Arg mutation site (Claim 18)"

Best Local Similarity 99.6%; Pred. No. 1 4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPPAPSYFQIAQMSBDNHISNTVSSQNDRERODNSRLGHEPLSNGRPOGNSR 60
 FT 1 MTELPPAPSYFQIAQMSBDNHISNTVSSQNDRERODNSRLGHEPLSNGRPOGNSR 60

FT Misc-difference 280 /note= "Glu280Ala mutation site (Claim 18)"
 FT 61 QVVEQDEREDEETLKQGAKHIMLFLFVTLGMMVYVATIKSVFVRKGQDOLIYPPTE 120
 FT 61 QVVEQDEREDEETLKQGAKHIMLFLFVTLGMMVYVATIKSVFVRKGQDOLIYPPTE 120

FT Misc-difference 285 /note= "Ala285Val mutation site (Claim 18)"
 FT 121 DTTIVGQALHSNAAAMISITWMTLWVTKRCYKTHAMLISSULLFPSP 180

FT Misc-difference 322 /note= "Leu322Val mutation site (Claim 18)"
 FT 121 DTENVGQALHSNTAAAMISIVWMTLWVLYKRCYKTHAMLISSULLFPSP 180

FT Misc-difference 384 /note= "Gly384Ala mutation site" 181 YLGAVFKTINAVDITWALLWNGVWGMISIHWKGPLRQOQAYLIMISALMAYPKY 240

FT Misc-difference 392 /note= "Leu392Val mutation site (Claim 18)"
 FT 181 YLGAVFKTINAVDITWALLWNGVWGMISIHWKGPLRQOQAYLIMISALMAYPKY 240

FT Domain 408 . 428 181 YLGAVFKTINAVDITWALLWNGVWGMISIHWKGPLRQOQAYLIMISALMAYPKY 240

FT /label= TM 241 LPWTNTAIIAVSVVDPVAVLCPKGFLRMVETAQERNETLPALIYSSTMWVMAE 300

FT /note= "transmembrane domain 8" 241 LPWTNTAIIAVSVVDPVAVLCPKGFLRMVETAQERNETLPALIYSSTMWVMAE 300

FT Misc-difference 410 /note= "Cys410Tyr mutation site (Claim 18)"
 FT 301 GDEPAQRKVSKNSKHNESTERESQDVAENDGGSEWEARQDHSIGPFRSPRA 360

FT 301 GDEPAQRKVSKNSKHNESTERESQDVAENDGGSEWEARQDHSIGPFRSPRA 360

FT 361 VQVSSSLAGDEPEERGVKGIGDFIIFSYLGVKQASATAGDWNNTIACVAILGLC 420

FT 361 VQVSSSLAGDEPEERGVKGIGDFIIFSYLGVKQASATAGDWNNTIACVAILGLC 420

FT 421 TULLAIFKKALPALPISITGELVYFATDYLQVQPMQDQAFHQFYI 467
 PR 421 TULLAIFKKALPALPISITGELVYFATDYLQVQPMQDQAFHQFYI 467

PR 02-JAN-1997; 97US-0034590P.
 PR 02-JAN-1997; 97US-0034590P.

XX 04-JUL-1997; 97WO-CA0000475.

XX 05-JUL-1996; 96US-0021573P.
 PR 12-JUL-1996; 96US-0021570P.
 PR 08-NOV-1995; 95US-0028895P.
 PR 02-JAN-1997; 97US-0034590P.

XX (UTOR) UNIV TORONTO GOVERNING COUNCIL.

XX (HSCR-) HSC RES & DEV LP.

XX PI St George- Hyslop PH, Fraser PE, Rommens JM;
 XX DR WPI; 1998-286355/25.

XX PA N-PSDB; AAV04666.

XX PT New isolated mutant presenilin-1 genes - useful for developing products for use in detection, diagnosis and therapy of Alzheimer's disease and for drug screening.

XX PT For use in detection, diagnosis and therapy of Alzheimer's disease and for drug screening.

XX PS Claim 1; Page 180-182; 238pp; English.

XX This polypeptide comprises human Presenilin-1 (PS1). Its amino acid sequence was deduced from an isolated cDNA clone (see AAV04666). Another hPS1 sequence (see AAW23965) results from alternative splicing of the hPS1 mRNA transcript. A murine PS1 homologue (see AAW23966) and a human presenilin-2 protein (see AAW23967) are also provided. Mutations in the PS-1 and PS-2 genes are linked to the development in humans of forms of familial Alzheimer's disease (FAD) and may be causative of other disorders, e.g. cognitive, intellectual, neurological or physiological disorders such as cerebral haemorrhage, schizophrenia, depression, mental retardation and epilepsy. Use of the nucleic acids and proteins comprising or derived from the presenilins is made in screening and diagnosing FAD, identifying cell lines and transgenic animals useful as models of FAD, methods for identifying substances that bind to, or modulate the activity of a presenilin protein, and methods for identifying substances that affect the interaction of a presenilin-interacting protein with a presenilin protein are also disclosed

XX Sequence 467 AA;

XX Query Match 99.5%; Score 2378; DB 2; Length 467;

XX The present invention describes a gene mutant animal having a non-human mutant presenilin gene. The mutant presenilin gene causes amino acid

Substitutions at 1 or more positions of 79, 82, 96, 115, 120, 135, 139, 143, 146, 163, 209, 213, 231, 235, 246, 250, 260, 263, 264, 267, 269, 280, 285, 286, 290, 318, 384, 392, 410, 425 and 436, with corresponding N-terminal's being e.g. R79V, V82L, A426 and P436S, particularly by replacing isoleucine by another amino-acid especially threonine. The gene mutant animals e.g. mice can be used as model animals for the study of human Alzheimer's diseases and to screen and evaluate substances as candidates for prevention and/or therapy of Alzheimer's diseases in patients. They can over-produce amyloid beta protein by the presenilin-1 gene to cause nerve cell death or peeling off in the hippocampus earlier. Such animals are being pathologically close to human patients with Alzheimer's diseases. The present sequence represents human presenilin-1, as given in the present invention sequence 467 AA;

Query Match 99.5%; Score 2378; DB 2; Length 467;

Best Local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELAPLSPYFQNAQMSEDNHLSTVRSQNDNRQERDRSIGHBPLSNRPGQNSR 60
Db 1 MTELAPLSPYFQNAQMSEDNHLSTVRSQNDNRQERDRSIGHBPLSNRPGQNSR 60
QY 61 QVVEQDEEDEEDEELTUKYGAHKVIMLFVPTLCHMVVWATIKSVSFYTRKDQIYIPPE 120
Db 61 QVVEQDEEDEEDEELTUKYGAHKVIMLFVPTLCHMVVWATIKSVSFYTRKDQIYIPPE 120
QY 121 DTETVGORALHSINAAIMSVIVMTILVILVLYKRYCKVIAHAWLISLLEPFSI 180
Db 121 DTETVGORALHSINAAIMSVIVMTILVILVLYKRYCKVIAHAWLISLLEPFSI 180
QY 181 YLGEVFKTIVNAVDYITVALLIMFGVGMISIHWKGPLRQLQYI 240
Db 181 YLGEVFKTIVNAVDYITVALLIMFGVGMISIHWKGPLRQLQYI 240
QY 241 LPENTAWLILAVISYDIAVLCIKGPKLMLVETAQERNETLPALIYSTMWLVNAAE 300
Db 241 LPENTAWLILAVISYDIAVLCIKGPKLMLVETAQERNETLPALIYSTMWLVNAAE 300
QY 301 GDPFAQRRYVSKNSKNAESTERESQDTAENDDGFREBEWAEORDSHIGPHRSTPESRAA 360
Db 301 GDPFAQRRYVSKNSKNAESTERESQDTAENDDGFREBEWAEORDSHIGPHRSTPESRAA 360
QY 61 QVVEQDEEDEEDEELTUKYGAHKVIMLFVPTLCHMVVWATIKSVSFYTRKDQIYIPPE 120
Db 61 QVVEQDEEDEEDEELTUKYGAHKVIMLFVPTLCHMVVWATIKSVSFYTRKDQIYIPPE 120
QY 121 DTETVGORALHSINAAIMSVIVMTILVILVLYKRYCKVIAHAWLISLLEPFSI 180
Db 121 DTETVGORALHSINAAIMSVIVMTILVILVLYKRYCKVIAHAWLISLLEPFSI 180
QY 181 YLGEVFKTIVNAVDYITVALLIMFGVGMISIHWKGPLRQLQYI 240
Db 181 YLGEVFKTIVNAVDYITVALLIMFGVGMISIHWKGPLRQLQYI 240
QY 241 LPENTAWLILAVISYDIAVLCIKGPKLMLVETAQERNETLPALIYSTMWLVNAAE 300
Db 241 LPENTAWLILAVISYDIAVLCIKGPKLMLVETAQERNETLPALIYSTMWLVNAAE 300
RESULT 7
AY23897 ID AAY23897 standard; protein; 467 AA.
XX AC AAY23897;
XX DT 27-SEP-1999 (first entry)
XX DE Amino acid sequence of the wild type human presenilin 1 (PS1) protein.
XX Human; presenilin 1; PS1; presenilin-binding protein; interacting domain; presenilin allele; Alzheimer's disease; senile dementia; psychiatric disease; schizophrenia; depression; neurological disease; stroke; cerebral haemorrhage.
XX OS Homo sapiens.
XX WO935501-A1.
XX PD 15-JUL-1999.

Query Match 99.5%; Score 2378; DB 2; Length 467;

Best Local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELAPLSPYFQNAQMSEDNHLSTVRSQNDNRQERDRSIGHBPLSNRPGQNSR 60
Db 1 MTELAPLSPYFQNAQMSEDNHLSTVRSQNDNRQERDRSIGHBPLSNRPGQNSR 60
QY 61 QVVEQDEEDEEDEELTUKYGAHKVIMLFVPTLCHMVVWATIKSVSFYTRKDQIYIPPE 120
Db 61 QVVEQDEEDEEDEELTUKYGAHKVIMLFVPTLCHMVVWATIKSVSFYTRKDQIYIPPE 120
QY 121 DTETVGORALHSINAAIMSVIVMTILVILVLYKRYCKVIAHAWLISLLEPFSI 180
Db 121 DTETVGORALHSINAAIMSVIVMTILVILVLYKRYCKVIAHAWLISLLEPFSI 180
QY 181 YLGEVFKTIVNAVDYITVALLIMFGVGMISIHWKGPLRQLQYI 240
Db 181 YLGEVFKTIVNAVDYITVALLIMFGVGMISIHWKGPLRQLQYI 240
QY 241 LPENTAWLILAVISYDIAVLCIKGPKLMLVETAQERNETLPALIYSTMWLVNAAE 300
Db 241 LPENTAWLILAVISYDIAVLCIKGPKLMLVETAQERNETLPALIYSTMWLVNAAE 300
QY 301 GDPFAQRRYVSKNSKNAESTERESQDTAENDDGFREBEWAEORDSHIGPHRSTPESRAA 360
Db 301 GDPFAQRRYVSKNSKNAESTERESQDTAENDDGFREBEWAEORDSHIGPHRSTPESRAA 360
QY 361 VOELSSSIAGEDBERGVKGPKLMLGDFPITFVSVLKGAKSATASGDWNTTACFVAILIGCL 420
Db 361 VOELSSSIAGEDBERGVKGPKLMLGDFPITFVSVLKGAKSATASGDWNTTACFVAILIGCL 420
QY 421 TLLIAFKCALPALPISITFGLVYFATDYLVQPFMDQLAHQFYI 467
Db 421 TLLIAFKCALPALPISITFGLVYFATDYLVQPFMDQLAHQFYI 467

RESULT 8
AAB07971 ID AAB07971 standard; protein; 467 AA.
XX AC AAB07971;

Query Match 99.5%; Score 2378; DB 2; Length 467;

Best Local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 (UTOR) UNIV TORONTO GOVERNING COUNCIL 09-JAN-1998; 98US-0070948P.
XX PI St George- Hyslop PH, Fraser PE;
XX DR WPI; 1999-419410/35.
PT Identifying substances that alter presenilin interactions useful for screening individuals for presenilin alleles associated with Alzheimer's disease - useful for diagnosis of Alzheimer's disease.

Query Match 99.5%; Score 2378; DB 2; Length 467;

Best Local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 (UTOR) UNIV TORONTO GOVERNING COUNCIL 09-JAN-1998; 98US-0070948P.
XX PI St George- Hyslop PH, Fraser PE;
XX DR WPI; 1999-419410/35.
PT Identifying substances that alter presenilin interactions useful for screening individuals for presenilin alleles associated with Alzheimer's disease - useful for diagnosis of Alzheimer's disease.

QY 61 QVVEQDEREDEELTLKIGAKHIVMLFPVTLQNVVWATIKSVSFTRKGQQLVTPFTE 12
 Db 61 QVTEQDESEDEETLKGAKHIVMLFPVTLQNVVATIKSVSFTRKGQQLVTPFTE 12
 QY 121 DTETVGORALHSINAAIMISIVWMTLILVLYKRCYKTHAMITISSLLLFFPSFI 18
 Db 121 DTETVGORALHSINAAIMISIVWMTLILVLYKRCYKTHAMITISSLLLFFPSFI 18
 QY 181 YGEVFKTYNAVDYTIVALLWNGGGMISIHWKGPLRQAVYIMISALMAVFIY 24
 Db 181 YGEVFKTYNAVDYTIVALLWNGGGMISIHWKGPLRQAVYIMISALMAVFIY 24
 QY 241 LPWTMILAVTSDYDVAVLKGPIRMLVETQERNETLPALIYSSNMVWMAE 30
 Db 241 LPWTMILAVTSDYDVAVLKGPIRMLVETQERNETLPALIYSSNMVWMAE 30
 QY 301 GDEBARQRSVSKNSKNAESTERSQDTVAENDGGSEHWEAQRSQHGLPERSTPESRAA 36
 Db 301 GDEBARQRSVSKNSKNAESTERSQDTVAENDGGSEHWEAQRSQHGLPERSTPESRAA 36
 QY 361 VQELESSSTLAGEDPERCVKLGIGDFPYSVNGKASATAGDWNTIACTVAILGLCL 42
 Db 361 VQELESSSTLAGEDPERCVKLGIGDFPYSVNGKASATAGDWNTIACTVAILGLCL 42
 QY 421 TLLIAFKKALPALISITFGIVFVFPATDYLWQPFMDQLAHFQFYI 467
 Db 421 TLLIAFKKALPALISITFGIVFVFPATDYLWQPFMDQLAHFQFYI 467
 421 TLLIAFKKALPALISITFGIVFVFPATDYLWQPFMDQLAHFQFYI 467

RESULT 10

AAG63916
 ID AAG63916 standard; protein; 467 AA.
 XX
 AC AAG63916;
 XX
 DT 29-OCT-2001 (first entry)
 DE Amino acid sequence of human presenilin 1.
 KW KIAA0253; presenilin; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200167109-A1.
 PD 13-SEP-2001.
 XX
 PF 09-MAR-2001; 2001WO-GB001057.
 XX
 PR 10-MAR-2000; 2000GB-00008894.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Hale RS, Rowley A, Blackstock W;
 DR WPI; 2001-522960/57.
 DR N-PSDB; AAB74993.

XX

PT Identifying a modulator of presenilin function by determining the ability of presenilin to bind to a KIAA0253 polypeptide in the presence and absence of a test compound, useful in the treatment or prophylaxis of Alzheimer's disease.

CC Disclosure; Page 40-41; 48pp; English.

CC

CC The present sequence represents human presenilin 1. KIAA0253 binds to presenilin. The specification describes a method of identifying a modulator of presenilin function or KIAA0253 function. The method comprises determining presenilin activity or KIAA0253 activity in the presence and absence of a test compound where presenilin activity is determined by its ability to bind to KIAA0253. A modulator of presenilin or KIAA0253 polypeptide is useful in the manufacture of a medicament for

the treatment or prophylaxis of Alzheimer's disease. The KIAA0253 polynucleotide and KIAA0253 Polypeptide are useful in the treatment, prophylaxis or diagnosis of Alzheimer's disease

PT McCarthy, J., Cordell, B;

XX

DR

XX

WPI: 2001451872/48.
N-PSDB; AAE05466.

PT

XX

PT

XX

PT

XX

PT

XX

PT

XX

PS

XX

Claim 4; Page 60-61; 66pp; English.

The invention relates to human Par-4 protein, presenilin protein (PS1 and PS2) and their corresponding DNA molecules. The invention also relates to a method for identifying inhibitors of neuronal degeneration, comprising co-transferring eukaryotic host cells expressing presenilin (PS), with a Par-4 DNA, and an NF-kappa B dependent reporter construct, exposing the cotransfected cells to a candidate molecule and monitoring the ability of the candidate molecule to induce NF-kappa B activation. Presenilin proteins participate in nuclear factor kappa B (NF-kappa B) signalling and activation. The inhibitors of neuronal degeneration are useful for treating neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and also for treating peripheral neuropathies, motorneuron disorders such as amyotrophic lateral sclerosis (ALS), Bell's palsy and various conditions involving spinal muscular atrophy and paralysis. The present sequence is human presenilin (PS1) protein

XX

XX

CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

Query Match 99.5%; Score 2378; DB 5; Length 467; Best local Similarity 99.6%; Pred. No. 1.4e

QY 241 LPENTAWLILAVISVYDLYVALCIGKPLRMVLTQERNETLPALIYSSTMWLNMAE 300
 QY 241 LPENTAWLILAVISVYDLYVALCIGKPLRMVLTQERNETLPALIYSSTMWLNMAE 300
 Db 301 GDPAAQRYSKNSKNAESTERESQDTVAENDGGFSEWEAQRSWEDLSGPHSTPSRAA 360
 QY 301 GDPAAQRYSKNSKNAESTERESQDTVAENDGGFSEWEAQRSWEDLSGPHSTPSRAA 360
 Db 301 GDPAAQRYSKNSKNAESTERESQDTVAENDGGFSEWEAQRSWEDLSGPHSTPSRAA 360
 QY 361 VQELSSILAGEDBERGKLGDPFIVSFLVKGASATASGDWNTTACFVAILIGCL 420
 Db 361 VQELSSILAGEDBERGKLGDPFIVSFLVKGASATASGDWNTTACFVAILIGCL 420
 QY 421 TLLIAIFKKALPALPISITFLGLVYFATDYLQOPMDQLAHQFYI 467
 Db 421 TLLIAIFKKALPALPISITFLGLVYFATDYLQOPMDQLAHQFYI 467
 RESULT 13
 AAU9416 AAU9416 standard; protein; 467 AA.
 XX AC AAU9416;
 XX DT 02-JUL-2002 (first entry)
 DE Human presenilin-1, PS-1.
 XX KW Human; integrin-linked kinase; ILK; presenilin-1; protein kinase B; PKB;
 KW Gamma secretase; apoptosis; Alzheimer's disease; PS-1; nootropic;
 KW neuroprotective; cytostatic; cancer.
 XX OS Homo sapiens.
 PN WO200222862-A2.
 PD 21-MAR-2002.
 XX XX PR 12-SEP-2001; 2001WO-GB004094.
 PR 12-SEP-2000; 2000GB-00022333.
 XX PA (GLAX) GLAXO GROUP LTD.
 XX PI Hiles ID, Ellis C;
 XX DR WPI; 2002-351896/38.
 XX PT Identifying agent that modulates interaction between integrin-linked kinase and presenilin-1, useful for treating Alzheimer's disease, and identifying agent that modulates protein kinase B or gamma secretase activity.
 XX PS Disclosure; Page 43-45; 53PP; English.
 XX CC The invention relates to identifying an agent modulating interaction between integrin-linked kinase (ILK) and presenilin-1 (PS1) comprising providing ILK, PS1 or their functional variants, as first and second components respectively, contacting the components in the presence of a test agent under conditions that in absence of the agent, would permit the components to interact and determining whether the agent is capable of modulating the interaction between the components. Also included are the method above where the components are protein kinase beta (PKB), gamma secretase or their functional variants, test kits for carrying out the methods and an agent identified by the methods. The methods are used for identifying an agent that modulates interaction between ILK and PS1, or PKB or gamma-secretase. The agent has therapeutic applications in treating humans or animals, for treating a host suffering from a condition associated with an interaction between ILK and PS1, activity of PKB, activity of gamma-secretase, apoptosis, cancer and Alzheimer's disease. The agent is also useful for manufacturing a medicament for use in treatment of the above mentioned conditions. The present sequence represents human presenilin-1, PS-1.
 XX SQ Sequence 467 AA;
 Query Match 99.5%; Score 2378; DB 5; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233; Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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 Db 1 MTELPAVLSPVQNAQMSEDNHLNTVRSONDRERQENDRRSLGHPPBPLSNGPQHNR 60
 QY 61 QVQEDEDEBLLTQGAKHVMIFVPTILCMVWATKSYSPYTRKDQQLYTPFRE 120
 Db 61 QVQEDEDEBLLTQGAKHVMIFVPTILCMVWATKSYSPYTRKDQQLYTPFRE 120
 QY 121 DTETVQGRALHSILNAIMSIVVINTILWLYKRCRKHAWLISLULPPTI 180
 Db 121 DTETVQGRALHSILNAIMSIVVINTILWLYKRCRKHAWLISLULPPTI 180
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 QY 241 LPENTAWLILAVISVYDLYVALCIGKPLRMVLTQERNETLPALIYSSTMWLNMAE 300
 Db 241 LPENTAWLILAVISVYDLYVALCIGKPLRMVLTQERNETLPALIYSSTMWLNMAE 300
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 Db 301 GDPAAQRYSKNSKNAESTERESQDTVAENDGGFSEWEAQRSWEDLSGPHSTPSRAA 360
 QY 361 VQELSSILAGEDBERGKLGDPFIVSFLVKGASATASGDWNTTACFVAILIGCL 420
 Db 361 VQELSSILAGEDBERGKLGDPFIVSFLVKGASATASGDWNTTACFVAILIGCL 420
 QY 421 TLLIAIFKKALPALPISITFLGLVYFATDYLQOPMDQLAHQFYI 467
 Db 421 TLLIAIFKKALPALPISITFLGLVYFATDYLQOPMDQLAHQFYI 467
 RESULT 14
 AAQ18049 AAQ18049 standard; protein; 467 AA.
 XX AC AAQ18049;
 XX DT 02-SEP-2002 (first entry)
 DE Presenilin Protein.
 XX KW Sel-12; presenilin; neuronal disorder; familial Alzheimer's disease; amyloid precursor protein; APP.
 XX OS Unidentified.
 PN US6376239-B1.
 XX PD 23-APR-2002.
 XX PF 04-APR-1997; 97US-00832867.
 XX PR 04-APR-1997; 97US-00832867.
 XX PA (ELEG-) ELEGENE GMBH.
 XX PI Baumeister R;
 XX DR WPI; 2002-478281/51.
 XX DR N-PSDB; AAI47323.
 XX PT Isolated DNA molecule comprising promoter of the sel-12 gene from Caenorhabditis elegans operably linked to heterologous gene, directs expression in neural cells and is useful to develop drugs to treat neuronal disorders.

Fri Apr 9 06:19:30 2004

us-09-785-474a-30.rag

Page 12

Db 421 TLLIAIFRKALPALPISITFGLVFYPATDYLVQPFMDQLaPHQFYI 467

Search completed: April 8, 2004, 16:56:31
Job time : 62 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Om protein - protein search, using sw model

Run on: April 8, 2004, 16:58:26 ; Search time 47 Seconds
(Without Alignments)

2612.596 Million cell updates/sec

Title: US-09-785-474a-30

Perfect score: 2391

Sequence: 1 MTELPAPISYFQNAQMSEDN. ATDYLVQPFMQLAFHQFYI 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgmn_6/prodata_1/pupaa/US07_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

RESULT 1
US-09-785-474-30
Sequence 30, Application US/09785474
Patent No. US2001002626A1
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
NAME: WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005 3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-Aug-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-Aug-1995

ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

APPLICATION NUMBER: 0609.4180002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2560

TELEFAX: 202-371-2540

16 1452 60.7 448 13 US-10-071-900-2 Sequence 2, Appli
17 1452 60.7 448 14 US-10-293-000-6 Sequence 6, Appli
18 1444 60.4 448 9 US-09-54-999-6 Sequence 6, Appli
19 1444 60.4 448 14 US-10-221-234-6 Sequence 6, Appli
20 1444 60.4 448 15 US-10-417-422-6 Sequence 1, Appli
21 1444 60.4 448 15 US-09-985-035-1 Sequence 8, Appli
22 798.5 33.4 180 9 US-09-923-153-8 Sequence 60796, A
23 653 27.3 354 12 US-10-425-114-60796 Sequence 47501, A
24 552.5 23.1 491 12 US-10-425-114-60796 Sequence 30637, A
25 552.5 23.1 491 14 US-10-029-986-31637 Sequence 1227, Ap
26 377 15.8 14 US-09-925-299-1227 Sequence 1227, Ap
27 365 15.3 101 10 US-09-925-299-1227 Sequence 11, Appli
28 365 15.3 101 10 US-09-925-299-1227 Sequence 16783, A
29 362.5 15.2 129 14 US-10-051-767-11 Sequence 10, Appli
30 361.5 15.1 131 14 US-10-051-767-10 Sequence 12, Appli
31 335 14.0 210 14 US-10-051-767-12 Sequence 16991, Sequence 38056, A
32 328.5 10.2 233 12 US-10-424-99-16951 Sequence 7, Appli
33 299 12.5 156 14 US-10-051-767-7 Sequence 6, Appli
34 299 12.5 166 14 US-10-051-767-13 Sequence 209024, Sequence 203174,
35 278.5 11.6 177 12 US-10-424-99-196783 Sequence 28604, A
36 246 10.3 74 14 US-10-051-767-9 Sequence 8, Appli
37 246 10.3 74 14 US-10-051-767-15 Sequence 14, Appli
38 243.5 10.2 65 9 US-09-84-767-38056 Sequence 2379, Ap

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TOPOLGY: linear

TYPE: amino acid

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-785-474-30

Query Match 100.0%; Score 2391; DB 9; Length 467; Best Local Similarity 100.0%; Pred. No. 1.5e-20; Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELAPALSYONAQSNDHLSNTVRSQDNRERHNDRSRSLGHPEPLNSRQGNSR 60

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Db 61 QVQEDEEDEBELLTKYGAKEVIMLFPUVPLCMVWVATKSVSFYTRKDQOLIYTPTE 120

QY 121 DRETGVGRALHSILNAIMSVIVMVTILLVLYKRCYKTHAWLILSSLLPFSP1 180

Db 121 DRETGVGRALHSILNAIMSVIVMVTILLVLYKRCYKTHAWLILSSLLPFSP1 180

QY 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHNGKPLRQLQAVLIMISALMVFVY 240

Db 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHNGKPLRQLQAVLIMISALMVFVY 240

QY 241 LPETWIAILAVISVVDLAVLCLKPRLMVETAQERNETLPALIYSTMWLVMNAE 300

Db 241 LPETWIAILAVISVVDLAVLCLKPRLMVETAQERNETLPALIYSTMWLVMNAE 300

QY 301 GDPEAQGRVSKNSKNAESTERESDQTVAENDGGSEEWQAQDSHLGPRSTESAA 360

Db 301 GDPEAQGRVSKNSKNAESTERESDQTVAENDGGSEEWQAQDSHLGPRSTESAA 360

QY 361 VQELSSSILAGEDPEERGVKLGIGDFIYFVSYLVGKASATSGDWNNTIACFVAILIGCL 420

Db 361 VQELSSSILAGEDPEERGVKLGIGDFIYFVSYLVGKASATSGDWNNTIACFVAILIGCL 420

QY 421 TLLIAFKKALPALPISITGLVYFATDYLVOPFMQDQPHOFYI 467

Db 421 TLLIAFKKALPALPISITGLVYFATDYLVOPFMQDQPHOFYI 467

RESULT 2 US-09-785-474-2

Sequence 2, Application US/09785474
; Patent No. US2001012626A1

GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH

WASCO, WILMA

TITLE OF INVENTION: Genetic Alterations Related To Familial
NUMBER OF SEQUENCES: 32CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/706,344

FILING DATE: 30-AUG-1996

APPLICATION NUMBER: 60/003,054

FILING DATE: 31-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0609.4180002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

QY 100.0%; Score 2391; DB 9; Length 467; Best Local Similarity 99.7%; Pred. No. 1.5e-20; Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELAPALSYONAQSNDHLSNTVRSQDNRERHNDRSRSLGHPEPLNSRQGNSR 60

Db 1 MTELAPALSYONAQSNDHLSNTVRSQDNRERHNDRSRSLGHPEPLNSRQGNSR 60

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Db 61 QVQEDEEDEBELLTKYGAKEVIMLFPUVPLCMVWVATKSVSFYTRKDQOLIYTPTE 120

QY 121 DRETGVGRALHSILNAIMSVIVMVTILLVLYKRCYKTHAWLILSSLLPFSP1 180

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QY 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHNGKPLRQLQAVLIMISALMVFVY 240

Db 181 YLGEVFKTYNVAVDYITVALLIWNFGVGMISIHNGKPLRQLQAVLIMISALMVFVY 240

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Db 301 GDPEAQGRVSKNSKNAESTERESDQTVAENDGGSEEWQAQDSHLGPRSTESAA 360

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Db 361 VQELSSSILAGEDPEERGVKLGIGDFIYFVSYLVGKASATSGDWNNTIACFVAILIGCL 420

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RESULT 3 US-09-785-474-32

Sequence 32, Application US/09785474

; Patent No. US2001012626A1

GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH

WASCO, WILMA

TITLE OF INVENTION: Genetic Alterations Related To Familial
NUMBER OF SEQUENCES: 32CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA

ZIP: 20005-3934
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

PATENT IN: Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996

APPLICATION NUMBER: 60/03,054
FILING DATE: 31-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679
REFERENCE DOCKET NUMBER: 0609-4180002

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-785-474-32

Query Match 99.5%; Score 2378; DB 9; Length 467;
Best Local Similarity 99.6%; Pred. No. 1.2e-205; Indels 0; Gaps 0;
Matches 465; Conservative 0; Mismatches 2; Gaps 0;

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QY 61 QVVEQDDEBEDLTLYGAKHIVMLFVPUVLCMVVWATKSVSFYTRKDGQLYTPTE 120
Db 61 QVVEQDDEBEDLTLYGAKHIVMLFVPUVLCMVVWATKSVSFYTRKDGQLYTPTE 120
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Db 181 YLGEVFKTYNVAVIDYTVALIINWFGWGMISIHKGCPJRLQQAIVLIMALVFIY 240
QY 241 LPETWTALILAVISVVDLAVLCKGPRLMVETQERNTEFLPALIYSSPMWVLMMA 300
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Db 301 GPPEAQPRVSKNSKNAESTERESDQTAENDGFSSEEAQRISHLGHRSTBRAA 360
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Db 361 VQELSS9SLAGEDPERRGVKGJGLDFIYFVSYLNGKASATASGDWTTIACFVAILIGCL 420
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Db 241 LPETWTALILAVISVVDLAVLCKGPRLMVETQERNTEFLPALIYSSPMWVLMMA 300
RESULT 5 US-09-785-454A-3
; Sequence 3, Application US/09878454A
; Patent No. US20020064828A1
; GENERAL INFORMATION:
; APPICANT: Monteiro, et al.
; TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presenilin
; FILE REFERENCE: 4115-161
; CURRENT APPLICATION NUMBER: US/09/878,454A
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/210,939
; PRIOR FILING DATE: 2000-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent version 3.1
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-454A-3
Query Match 99.5%; Score 2378; DB 9; Length 467;

RESULT 4
US-09-754-949-4
; Sequence 4, Application US/09754949
; Patent No. US2002001539A1
; GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Tanzi, Rudolph E.
Schellenberg, Gerard D.
Wasco, Wilma
Levy-Jahad, Ephrat
Bird, Thomas D.
Gallas, David J.

TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADRESSE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Ave, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READEABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US1010180,781
FILING DATE: 24-Jun-2002
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Porter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 920010.571C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-9000
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-221-254-4

Query Match 99.5%; Score 2378; DB 14; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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1 MTEPAPLSYFQNAQMSBNHLSNTVRQNDRERQHNDRSLGHEPEPLSNRPGNSR 60

QY 61 QVTEQDEEEDEELTLYGAKHVMFLFVPTLCKVWVATIVSVEYTRKQDQIYPTF 120
61 QVVEODEEEDEELTLYGAKHVMFLFVPTLCKVWVATIVSVEYTRKQDQIYPTF 120

Db 121 DTETVGQRALHSINAAMISVIVMUTLILVLYKIRYKVTHAWLISLILLFFPSI 180
121 DTETVGQRALHSINAAMISVIVMUTLILVLYKIRYKVTHAWLISLILLFFPSI 180

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181 YLGEVFKTYNAVDYTIVALLINFGVGMISHWKGPRLQAYLIMISALVALFYK 240

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QY 301 GDEBAQRVSKNSKNAESTERESQDTWAENDGGFSEWEAQRDHGPRTSPSRA 360
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Db 361 VOELSSSLAGEDPEERYKLGDFITSVLUGKASTAGDWNTTACFVAILIGCL 420
361 VOELSSSLAGEDPEERYKLGDFITSVLUGKASTAGDWNTTACFVAILIGCL 420

QY 421 TLLIAFKKALPALPISITGLVYFATDYLQPEMDQLAHQFYI 467
421 TLLIAFKKALPALPISITGLVYFATDYLQPEMDQLAHQFYI 467

Db 301 GDEPAQRVSKNSKNAESTERESQDTWAENDGGFSEWEAQRDHGPRTSPSRA 360
301 GDEPAQRVSKNSKNAESTERESQDTWAENDGGFSEWEAQRDHGPRTSPSRA 360

RESULT 9

US-10-180-781-3

; Sequence 3, Application US/10180781

; Publication No. US2003016088041

APPLICANT: TANZI, RUDOLPH
WASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial
Alzheimer's Disease

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC

COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 20-FEB-2001

ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609.4180002

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-785-474-4

Query Match 99.5%; Score 2378; DB 15; Length 467;
Best Local Similarity 99.6%; Pred. No. 2,28-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MTELAPLSVQNAQMSEDNHLNSNTVRSQNDNRQERDRRSIGHPEPLSNGRPGQNSR 60

Qy 1 MTELAPLSVQNAQMSEDNHLNSNTVRSQNDNRQERDRRSIGHPEPLSNGRPGQNSR 60

Db 1 QVVEQDEBEDBELTLYGAKRVMIFPVPTLCMVWVATKSVSFYTTRKDQOLYTPFTE 120

Qy 1 QVVEQDEBEDBELTLYGAKRVMIFPVPTLCMVWVATKSVSFYTTRKDQOLYTPFTE 120

Db 61 QVVEQDEBEDBELTLYGAKRVMIFPVPTLCMVWVATKSVSFYTTRKDQOLYTPFTE 120

Qy 121 DTETVGORALHSILNAIMISVIVNTILLVLYKRCYKVIHAWLISLILLFFPSFI 180

Db 121 DTETVGORALHSILNAIMISVIVNTILLVLYKRCYKVIHAWLISLILLFFPSFI 180

Qy 181 YLGEVFKTYNAVDTYVALLIINFGVGWVMSIHKGPRLQYLMISALMVFYK 240

Db 181 YLGEVFKTYNAVDTYVALLIINFGVGWVMSIHKGPRLQYLMISALMVFYK 240

Qy 241 LPETWAWLILAVISTYDVALCILKGPIMLVQAERETPLALITYSTMWLNMAE 300

Db 241 LPETWAWLILAVISTYDVALCILKGPIMLVQAERETPLALITYSTMWLNMAE 300

Qy 301 GPDEAQRRVSKNSKNAESTERESQDTVAENDGGFSEWAQDSDHGPHRSTPESRA 360

Db 301 GPDEAQRRVSKNSKNAESTERESQDTVAENDGGFSEWAQDSDHGPHRSTPESRA 360

Qy 361 VOELSSILAGEDPBERGVKGIGPFTSVLVGKASATASGDWNTTACFVALIGCL 420

Db 361 VOELSSILAGEDPBERGVKGIGPFTSVLVGKASATASGDWNTTACFVALIGCL 420

Qy 421 TLLIAIFKALPALPISITFGVLYVATDLYQPFMDLAFQFYI 467

Db 421 TLLIAIFKALPALPISITFGVLYVATDLYQPFMDLAFQFYI 467

RESULT 11
US-09-785-474-4
; Sequence 4, Application US/09785474
; Patent No. US2001012026A1
; GENERAL INFORMATION:

RESULT 14 ; FILE REFERENCE: 4115-161
 US-10-293-000-5 ; CURRENT APPLICATION NUMBER: US/09/878,454A
 ; Sequence 5, Application US/10293000
 ; Publication No. US20030175278A1 ; CURRENT FILING DATE: 2001-06-11
 ; GENERAL INFORMATION ; PRIOR APPLICATION NUMBER: 6/210,939
 ; ; NUMBER OF SEQ ID NOS: 26
 ; ; SOFTWARE: Patentin version 3.1
 ; ; SEQ ID NO: 1
 ; ; LENGTH: 448
 ; ; TYPE: PRT
 ; ; ORGANISM: Homo sapiens
 ; ; US-10-293-000-5
 ; ;
 ; ; Query Match 94.8%; Score 2266; DB 14; Length 467;
 ; ; Best Local Similarity 94.6%; Pred. No. 2.6e-195; Matches 442; Conservatve 12; Mismatches 13; Indels 0; Gaps 0;
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 ; ; Matches 304; Conservatve 40; Mismatches 80; Indels 42; Gaps 8;
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 ; ; QY 1 MTELAPLSTFONAQNMSDHNLSNVRQDNRERQHNDRRSLGHPEPLSNRPGQNSR 60 ; ;
 ; ; Db 1 MTELAPLSTFONAQNMSDHNLSNVRQDNRERQHNDRRSLGHPEPLSNRPGQNSR 60 ; ;
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 ; ; QY 61 QVVEDEEEDEBELTLYKAGKRVIMFVPUVTCMVWVATKSVFTRKGQLYTPTE 120 ; ;
 ; ; Db 61 PVVERDEEEDEBELTLYKAGKRVIMFVPUVLCMVWVATKSVFTRKGQLYTPTE 120 ; ;
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 ; ; QY 121 DTETYGQRALKSINAKAIMSVIVNTILLVLYKRYCTKTHAWLILSSLLFFPT 180 ; ;
 ; ; Db 121 DTETYGQRALKSINAKAIMSVIVNTILLVLYKRYCTKTHAWLILSSLLFFPT 180 ; ;
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 ; ; QY 181 YLGEVKTKYNAVDYDITVALLWNGVGMISIHWKPLRQOAVIMISALMAYRKY 240 ; ;
 ; ; Db 181 YLGEVKTKYNAVDYDITVALLWNGVGMISIHWKPLRQOAVIMISALMAYRKY 240 ; ;
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 ; ; Db 181 YLGEVKTKYNAVDYDITVALLWNGVGMISIHWKPLRQOAVIMISALMAYRKY 240 ; ;
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 ; ; QY 241 LPWTAWLILAVISYDVLWVCLKGPLRMLVETAQERNETLPALIYSTMWLNMAE 300 ; ;
 ; ; Db 241 LPWTAWLILAVISYDVLWVCLKGPLRMLVETAQERNETLPALIYSTMWLNMAE 300 ; ;
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 ; ; QY 301 GDPEAQRRVKNSKRNARETERESQDTVAENDGGFSEEWBAORDSHLGHPRSTPESRA 360 ; ;
 ; ; Db 301 GDPEAQRRVKNSKRNARETERESQDTVAENDGGFSEEWBAORDSHLGHPRSTPESRA 360 ; ;
 ; ;
 ; ; QY 361 VQELSSSILGEGDPBERGVVLGLGDFIFVSSVLVGKASATASGDNTTACFVAILIGCL 420 ; ;
 ; ; Db 361 VQELSSSILGEGDPBERGVVLGLGDFIFVSSVLVGKASATASGDNTTACFVAILIGCL 420 ; ;
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 ; ; QY 421 TILLIAIFKALPALPISITGLVYFATDYLVQPFMDQIAFHOFYI 467 ; ;
 ; ; Db 421 TILLIAIFKALPALPISITGLVYFATDYLVQPFMDQIAFHOFYI 467 ; ;
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 ; ; RESULT 15 ;
 ; ; US-09-878-454A-1 ;
 ; ; Sequence 1, Application US/09878454A
 ; ; Patent No. US2003006428A1
 ; ; GENERAL INFORMATION
 ; ; APPLICANT: Monteiro, et al.
 ; ; TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presenilin